

Original Contribution

Invasive American Mink: Linking Pathogen Risk Between Domestic and Endangered Carnivores

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Abstract: Infectious diseases, in particular canine distemper virus (CDV), are an important threat to the viability of wild carnivore populations. CDV is thought to be transmitted by direct contact between individuals; therefore, the study of species interactions plays a pivotal role in understanding CDV transmission dynamics. However, CDV often appears to move between populations that are ecologically isolated, possibly through bridge hosts that interact with both species. This study investigated how an introduced species could alter multihost interactions and act as a bridge host in a novel carnivore assemblage of domestic dogs (*Canis familiaris*), invasive American mink (*Neovison vison*), and threatened river otters (*Lontra provocax*) in southern Chile. We found that rural dogs interact with mink near farms whereas in riparian habitats, minks and river otters shared the same latrines with both species visiting sites frequently within time intervals well within CDV environmental persistence. No interactions were observed between dogs and otters at either location. Both dog and mink populations were serologically positive for CDV, making the pathogen transfer risk to otters a conservation concern. Altogether, introduced mink in this ecosystem have the potential to act as bridge hosts between domestic dogs and endangered carnivores.

Keywords: bridge host, *Neovison vison*, *Lontra provocax*, *Canis familiaris*, interactions, distemper

INTRODUCTION

Infectious diseases are a growing threat for biodiversity conservation (Daszak et al. 2000; Lafferty and Gerber 2002). In recent years, several lines of evidence strongly suggest that a wide range of species, from plants (Anderson

et al. 2004) to bats (Blehert et al. 2009), and from amphibians (Skerratt et al. 2007) to large carnivores (Murray et al. 1999) are suffering important population setbacks due to the emergence or reemergence of infectious diseases. Anthropogenic change is thought to be an important driver of infectious disease emergence (Daszak et al. 2000; Dobson and Foufopoulos 2001; Woolhouse and Gowtage-Sequeria 2005). Most research to date has focused on how human encroachment into natural habitats and

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habitat degradation alters human–wildlife contact (e.g., bushmeat hunting, urbanization) (e.g., Brashares et al. 2004; McDonald et al. 2008). One anthropogenic driver that bears further consideration and investigation is the impact that invasive species may have on disease risk for vulnerable wildlife.

Invasive species can carry diseases of concern to vulnerable wildlife when they move into their habitat (Daszak et al. 2001; Hatcher et al. 2012). Therefore, they pose a risk for disease transfer to wildlife populations. Well-documented cases include the transmission of parapox virus from invasive gray squirrels (*Sciurus carolinensis*) to red squirrels (*S. vulgaris*) in the United Kingdom (Tompkins et al. 2003), or the fungal pandemic, *Batrachochytrium dendrobatidis*, in amphibians associated with the global trade of African clawed frogs (*Xenopus laevis*) (Weldon et al. 2004). In some cases, disease transmission may be direct as the introduced species invades the native species' habitat (Tompkins et al. 2003; Weldon et al. 2004). However, the arrival of invasive species could also alter the dynamics of interactions within the host communities and therefore have consequences in terms of the risk of multi-host pathogen disease transfer. This is of major interest when two species that are segregated in terms of habitat use and have few interactions become functionally connected by a third species whose new habitat preferences overlap the two otherwise unconnected populations. This, in turn, would create new multihost pathogen dynamics with the invasive species potentially acting as a bridge host between the two populations. A “bridge host” (or bridging host) is a host that allows disease transmission between two otherwise unconnected host populations or, more generally, between transmission cycles (see also Jenkins et al. 2011).

Domestic animals also play an important role in infectious disease dynamics. In some regions, domestic animals can reach high densities due to anthropogenic food resources, shelter, and veterinary care (Diamond and Ordunio 1997; Wolfe et al. 2007). Therefore, domestic animals may act as amplifiers of infectious diseases and serve as a source of pathogen spill-over for diseases that could not otherwise be maintained by rare native species (Grenfell and Dobson 1995; Woodroffe 1999). Pathogen spill-over can occur in two directions when domestic animals and wild species are in close proximity (Lembo et al. 2008). Disease transmission can occur from wildlife to domestic animals when wildlife abundance is artificially high as with transmission of bovine tuberculosis between food supplemented deer and domestic cattle in Michigan

(Schmitt et al. 2002) or the emergence of Hendra virus associated with the dramatic increase in urban flying fox colonies in Australia and transmission to domestic horses (Plowright et al. 2011). Disease spill-over can also occur from domesticated animals to wildlife (e.g., Woodroffe 1999; Daszak et al. 2000; Lembo et al. 2008). When this situation occurs in areas of importance for wildlife conservation, domestic animals can be a potential risk for threatened species. Examples include the transmission of *Toxoplasma gondii* from domestic cats (*Felis catus*) to sea otters (*Enhydra lutris*) (Miller et al. 2002), rabies from domestic dogs (*Canis familiaris*) to Ethiopian wolves (*Canis simensis*) (Sillero Zubiri et al. 1996), or *Pasteurella* sp. from domestic sheep (*Ovis aries*) to bighorn sheep (*O. canadensis*) (Foreyt and Jessup 1982).

One of the multihost pathogens of major concern for wild carnivores is the canine distemper virus (CDV). CDV is a morbillivirus that infects most mammalian carnivores and is characterized by its high lethality (Appel 1987; Deem et al. 2000). In recent years, CDV has been recognized as an important threat to wildlife since outbreaks have been implicated in declines of threatened and charismatic species such as the gray wolf (*Canis lupus*) (Almberg et al. 2012), black-footed ferret (*Mustela nigripes*) (Williams et al. 1988), African wild dog (*Lycaon pictus*) (Alexander and Appel 1994), or African lion (*Panthera leo*) (Roelke-Parker et al. 1996). Transmission of CDV is thought to be primarily through direct contact, but under test conditions, the virus can survive from a few hours at 25°C to 14 days at 5°C (Shen and Gorham 1980). Transmission generally occurs through oronasal secretion but all bodily fluids can carry the virus (Haas and Barrett 1996) and can reach high levels in urine (Elia et al. 2006; Saito et al. 2006) and feces (Acton 2007). In wildlife, short-term indirect transmission through fomites has been postulated as a source of transmission with examples including lions and hyenas sharing carcasses (Craft et al. 2011) or virus survival in an underground burrow of the black-footed ferret (Thorne and Williams 1988). To our knowledge, the relative importance of fomites in CDV transmission or indirect transmission has not been studied.

We studied the dynamics of interactions and the risk of CDV transmission among three sympatric carnivore species in southern Chile: domestic dogs, invasive American minks (*Neovison vison*), and endemic Southern river otters (*Lontra provocax*). Our study was conducted in an area characterized by a temperate climate where the survival of CDV in the environment should be long. The Southern river

otter is classified as an endangered species (Sepúlveda et al. 2008) due to habitat degradation and human disturbance (Medina 1996; Medina-Vogel et al. 2003; Sepúlveda et al. 2007, 2009). Domestic dogs in southern Chile are common and are used for farm animal protection and household guarding (Sepúlveda et al. 2014). Rural dogs spend most of their time near human houses (Sepúlveda 2013), whereas otters rarely move away from rivers (Sepúlveda et al. 2007). Thus, dogs and otters should have a low interaction risk. The American mink was introduced to Chile and Argentina in the 1960s and escapees invaded southern South America (from 39° S to Tierra del Fuego) (Jaksic 1998; Jaksic et al. 2002). Mink use both aquatic and terrestrial habitats (Dunstone 1993). Minks visit otter latrines (Rodríguez-Jorquera and Sepúlveda 2011), and also get close to human houses—and consequently dogs—in rural areas of the region (Sepúlveda et al. 2014). We hypothesized that mink is an effective bridge host species that increases the risk of transmission of pathogens such as CDV from dogs to otters. To test this hypothesis, we used interviews and camera traps to determine dog–mink–otter interactions in areas surrounding farms and along the margin of rivers. At the same time, we tested mink and dogs for CDV titers to determine if these populations had been exposed to the virus.

METHODS

Study Area

The study was conducted in the Valdivian Temperate Forests of Southern Chile, specifically in the Chaihuín and Colún rivers (39°52'S, 73°25'W) (Fig. 1). The study site included areas surrounding the Alerce Costero National Park (24,694 ha; ACNP) and the Valdivian Coastal Reserve (50,530 ha; VCR). Near the border of these protected areas and along the Chaihuín River are the villages of Chaihuín (more connected to towns) and Cadillal Alto (more isolated) (Fig. 1). Mean annual rainfall is 2,500 mm and annual average temperature is 12°C (average minimum of the coldest month of the year: 5°C; average maximum of the hottest month of the year: 17°C) (Luebert and Plischoff 2005).

Measuring Inter-species Interactions

Interactions among the three species were assessed at two locations: (1) around households where domestic dogs

spend most of their time (Sepúlveda 2013), and (2) in riparian habitats where otters are likely to occur (Sepúlveda et al. 2007). To address interactions around households, we interviewed dog owners about dog–wildlife interactions. During January 2010, we interviewed 52 households in the area to determine: (1) the proportion of dog owners that observed at least one mink or otter around their households during the previous year, and (2) whether the dog owner observed at least one interaction between dogs and mink or dogs and otters. Dog–mustelid interactions reported by farmers were defined as those where the interviewee observed an actual contact such as a dog killing or harassing mustelids (see also Sepúlveda et al. 2014).

We used camera traps to determine if mink or dogs were interacting with river otters in riparian habitat. Specifically, we compared the frequency of dog, mink, and otter visits to otter latrines against visits to random sites along the edge of the river. We deployed 91 camera traps between December 2010 and April 2011 (Bushnell Trophy Cam, Bushnell Corporation, and Capture IR, Cuddeback) along the Chaihuín River ($n = 46$) and Colún River ($n = 45$) covering a total of 20 km of river. Cameras were removed and installed in a new location after approximately 16 days. Camera traps were set on all latrine sites ($n = 37$) that were previously located through an intensive survey of the riverbanks of both rivers (minimum distances between latrines: 55 and 69 m for Chaihuín and Colún rivers, respectively). We deployed camera traps during four trapping periods. We placed cameras at latrines and matched random sites using a subset of randomly selected sites during each trapping period until all selected sites were covered. Because otters spend most of their time within 10 m of rivers (Sepúlveda et al. 2007), 54 cameras were placed in randomly generated locations within 5 m from the shore and with at least 200 m between camera traps, including distance to latrine sites. At each camera site, we visually estimated the percentage of understory (<1 m height) within a 5-m radius pivoting around the spot pointed by the camera, which in the case of latrines was the point with most otter signs (modified from Depue and Ben-David 2010).

We defined interactions as two different species using the same site within a time interval between visits < 14 days (survival of virus in cold environment, Shen and Gorham 1980). We considered that otter latrines might increase the risk of indirect CDV transmission because otters concentrate scent marking at those sites (Kruuk 2006), and our preliminary observations strongly suggested

that other carnivores also used otter latrines. Scent marking involves behaviors such as sniffing, rolling, defecating, and urinating (Macdonald 1985), which may increase disease risk.

Mink Site Selection and Disease Transmission Risk

We used a negative binomial regression (Hilbe 2011) where the number of mink visits to a site was the response variable to test whether minks were selecting otter latrines. To account for the fact that some minks spent several minutes at the same trap site, we considered independent events those that were at least 3 h apart at the same site. We used the time of camera monitoring (days in log scale) as an offset because the duration of monitoring period varied by camera. We used four predictor variables to determine the probability of a mink visiting a particular site: type of site (latrine or random), understory vegetation (%), number of otter visits, and river site (Chaihuín River or Colún River). We used the number of otter visits to a site because we predicted that mink visits could be negatively affected if the particular site was also used by an otter (i.e., intraguild killing) (Donadio and Buskirk 2006; Simpson 2006). Understory vegetation and river site (Chaihuín or Colún) were included as habitat covariates. Model output was expressed as the incidence rate ratio (IRR), which corresponds to the ratio of the incidence rate (number of new mink visits) for a particular group (i.e., random site), divided by the incidence rate in the other group (i.e., latrine site) (Hilbe 2011). For model selection purposes we used the combination of all possible additive models considering the four predictor variables and the intercept only model. Models were ranked by AIC criteria corrected for small sample size (AICc). Selected models were those with a $\Delta AICc < 2$ (Burnham and Anderson 2002). We assessed the fit of the best model using χ^2 goodness of fit.

To determine the number of interactions with potential risk of CDV transmission among species, we quantified the number and time interval between visits of different species at each camera site. Mean, median, and range of days between visits were calculated in the following indirect interactions between species: mink followed by otter (mink \rightarrow otter), otter followed by mink (otter \rightarrow mink), dog followed by mink (dog \rightarrow mink), mink followed by dog (mink \rightarrow dog), dog followed by otter (dog \rightarrow otter), and otter followed by dog (otter \rightarrow dog).

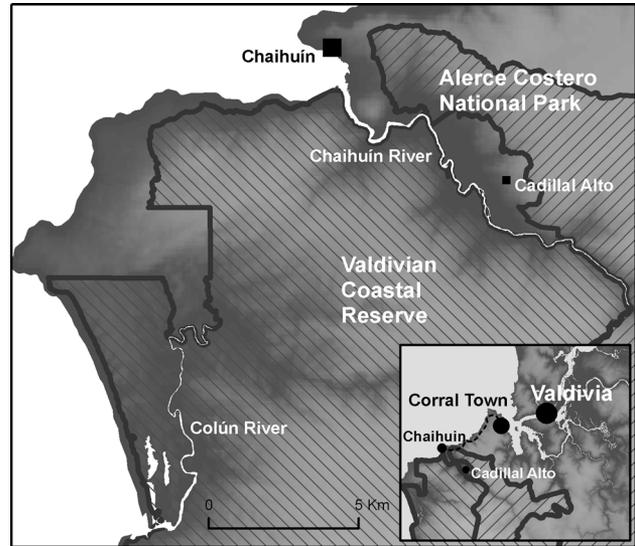


Figure 1. Study area showing the location of the Colún and Chaihuín rivers where camera traps were set up, and the location of the human settlements Chaihuín and Cadillal Alto, where domestic dogs were sampled for CDV testing. We collected serum samples from American mink in the Chaihuín river. *Inset map* shows the location of the study area in relation major human settlements including the city of Valdivia.

CDV Serology

Mink and dogs were tested for CDV antibody titers to specifically characterize the CDV disease transmission risk to otters. Between November 2009 and February 2010, we captured American minks ($n = 26$) at the Chaihuín River (Fig. 1) using cage traps (Tomahawk®, WI, USA). Traps were placed along a 10-km stretch of riverbank, baited with mackerel fish or chicken and checked twice per day for mink captures. All traps were located within 10 m of the shore with at least ~ 200 m between traps. Animals were sedated in the trap using an adapted protocol from Fournier-Chambrillon et al. (2003) with a combination of 10 mg/kg of ketamine (Ketamil®, 100 mg/ml, Ilium, Troy Laboratories, NSW 2164, Australia) and 0.025 mg/kg of medetomidine (Domitor®, 1 mg/ml, Pfizer, Madrid 28002, Spain) intra-muscularly. Once sedated, a 1.0 ml blood sample was collected via venipuncture of the jugular vein, placed in a serum-separating tube, and held at room temperature until processing. After sampling and data collection, the anesthesia was reversed with the antagonist Atipamezole (0.125 mg/kg i.m., Antisedan®, Pfizer, Madrid 28002, Spain) administered intra-muscularly. We considered mink to be juveniles when they had adult teeth

without abrasion and tartar, and adults otherwise (Fournier-Chambrillon et al. 2004).

In March 2010, we drew blood from at least one adult (>5 months) dog ($n = 60$) at each household sampled in Chaihuín and Cadillal Alto villages. Any household reporting a history of canine distemper vaccinations, including owners reporting vaccinations without specific knowledge of the type of vaccine (i.e., rabies or distemper) was excluded as well. This also applied to any dogs <5 months old to avoid false positives due to vaccine-induced or maternal antibodies (Chappuis 1998). Dog identification and age were provided by owners. Owners were also asked to characterize dogs into one of two categories: unrestricted (100% free roaming) or restricted (dogs kept some or all of the time indoors, in pens or on chains). Dogs were manually restrained and 2 ml of blood was drawn from the cephalic vein. Blood was processed as described for minks.

Dog and mink samples were transported to a field laboratory and centrifuged within 6 h of collection and serum transferred by pipetting to Eppendorf tubes to be stored. Both mink and dog serum samples were stored in a -18°C freezer in the field laboratory, transported on ice packs to the United States and stored at -70°C in a freezer prior to submission to the Veterinary Diagnostic Laboratory at Colorado State University. Seropositivity to CDV was analyzed using a microneutralization test (Appel 1987). Because the CDV serum test was not validated for mink we compared two cut-off values of 1:8 and 1:16 based on values used in previous studies (Almberg et al. 2009; Gowtage-Sequeira et al. 2009; Prager et al. 2013). For the dog serum samples, we used the recommendation of the laboratory, and a titer of $\geq 1:4$ was considered positive.

The association of seropositivity of CDV with identified risk factors was determined for dogs for the following variables: Age (juvenile: defined as ≤ 2 ; otherwise adult), site (Chaihuín or Cadillal), and dog management category (100% free roaming; otherwise restricted). Risk factors were determined using logistic regression (Agresti 2002). In this case, we were interested to test the association of predictors to CDV seropositivity from the global model without performing a model selection process. We assessed the goodness of fit of the model through the unweighted sum of squares test (Hosmer et al. 1997). Risk factors associated with CDV in mink were not determined because of the limited sample size ($n = 23$). Statistical analyses were performed using the software R (R Development Core Team 2011) using an α level = 0.05.

RESULTS

During the year prior to the interviews, 23% of respondents observed mink close to their households. Of these mink sightings, 42% involved at least one dog–mink interaction. Two dog–mink interactions resulted in the mink being killed by the dogs while in the remaining cases the mink escaped. In contrast, only 6% of dog owners saw southern river otters and none observed dog–otter interactions.

Minks, otters, and dogs were detected at 30, 17, and 3 camera sites, representing 97, 31, and 4 independent visits to these sites, respectively. The likelihood of mink visiting camera sites was influenced by site type (latrine/random) and river system (Chaihuín/Colún) based on a positive IRR (Table 1). Mink were more than four times more likely/day of camera trapping to visit a latrine site than a random site and nearly five times more likely/day of camera trapping to be seen at the Chaihuín camera trapping sites versus the Colún sites (Table 1). Habitat site characteristic (% understory vegetation) was not correlated to the number of mink visits to camera trap sites. Even though the numbers of otter visits were included in the second AIC model (Table 1), it did not have an association with the predictor variable as confidence intervals included the value 1.0.

All otter detections occurred at latrines. Co-use of sites by carnivores was detected at 10 camera sites. Of these, otters and minks were co-using eight camera sites, all of these latrines, representing 22.2% of the latrines surveyed and 47% of latrines visited by otters. Mink and dogs co-used two sites: one random and one latrine. In contrast, we did not detect co-use of any site by dogs and otters, although a dog was detected at a latrine. Cross-carnivore interactions were detected at camera trap sites between otter \rightarrow mink, mink \rightarrow otter, and dog \rightarrow mink (Table 2; Fig. 2). In addition, the median and average time between these interactions ranged from 1.2 to 1.7 days, well within the range of CDV environmental survival estimates (Table 2). We did not detect mink \rightarrow dog or dog \rightarrow otter interactions.

We captured 26 different minks in 49 trapping days representing 1,211 trap nights. Of these mink serum samples, three were not analyzed due to insufficient volume. Overall, CDV seroprevalence in mink was 39.1% (95% CI 20.4–61.2) using a titer cut-off of 1:8 and 21.7% (95% CI 8.2–44.2) using the 1:16 cut-off. Two mink cubs (<3 months) had positive CDV titers (1:16 and 1:512).

A total of 59 dogs were sampled for CDV testing. For dogs across all sites and ages, CDV seroprevalence was

Table 1. Model Selection for Variables Expected to Influence the Visitation of Minks

Model	K	AICc	Δ	w_i	Site (latrine)	River (Chaihuín)	Otter
Site + river	3	228.6	0.00	0.42	4.0 (1.4–13.7)	4.7 (1.6–15.8)	–
Site + river + otter	4	230.5	1.87	0.16	4.3 (1.4–15.0)	4.5 (1.5–15.4)	0.9 (0.5–1.6)

Models with little support ($\Delta\text{AICc} > 2$) are not shown. Parameter estimates are shown as incidence rate ratio and confidence intervals (in parenthesis) are shown for site (latrine/random), the river (Chaihuín/Colún), and for the number of otter visits (otter).

Table 2. Time Intervals of Different Directional Interactions Between Otter, Minks, and Dogs Detected at Camera Traps

	Mink → otter	Otter → mink	Dog → mink	Mink → dog	Dog → otter	Otter → dog
Number of events	8	6	2	0	0	0
Average (days)	4.0	3.9	1.2	–	–	–
Median (days)	1.7	1.5	1.2	–	–	–
Range (days)	0.6–16.5	0.6–4	0.2–2.3	–	–	–

Arrow indicates the sequence of the interaction between the indicated species.

41.6% (95% CI 29.3–55.0). Significant predictors of positive CDV titers in dogs were age, with older dogs having higher CDV prevalence than younger dogs, and river site, with dogs from Chaihuín having higher CDV seroprevalence than the more isolated Cadillal Alto (Table 3). There was no evidence supporting an effect of roaming restriction (Table 3). Four seropositive juvenile dogs (<2 years old) had titers ranging from 1:16 to 1:1,024.

DISCUSSION

Our study suggests that invasive species can theoretically increase disease risk to native species by acting as a “bridge host” between otherwise isolated native and domestic animals (Fig. 3). The diagnosis of CDV in urban dogs in Chile is common (López et al. 2009; Acosta-Jamett et al. 2011) including Valdivia, a city located close to the study site (Ernst et al. 1987). Furthermore, growing evidence suggests that it is also frequent in rural areas (Acosta-Jamett et al. 2011, this study). Dogs and otters were neither reported nor detected interacting in either the peri-farm or the river habitat, thus suggesting that these interactions are infrequent. In contrast, the introduced American mink interacted directly (harassment) and indirectly (co-use of latrines) with both otters and dogs. Furthermore, we recovered two mink carcasses, and the cause of deaths was attributed through necropsy to dog and river otter attacks, respectively (Sepúlveda pers. obs.). Indirect interactions in

latrines were separated by a median of approximately 2 days, an interval during which pathogens such as CDV can remain viable in the environment (Shen and Gorham 1980). This kind of co-use is comparable to other documented indirect interaction risks like sharing carcasses (Craft et al. 2011) and could lead to disease transmission through fomites.

Mink–other carnivore interactions were driven by different processes in the peri-farm and river systems. On farms, interactions were driven by dog–mink conflict and livestock guarding behavior (Sepúlveda et al. 2014), as previously reported in Spain (Zuberogoitia et al. 2006). Along rivers, minks showed clear preference for otter latrines relative to random sites (Table 1). Furthermore, there seem to be potential cross-species marking behaviors with mink marking closely following otter marking and vice versa (Fig. 2). Alternatively, both species could be selecting the same marking sites because of favorable habitat conditions for marking, likely the basis for the latrine site being established in the first place. Independent of its ultimate causes, this kind of cross-species interaction behavior merits further study as a mechanism of disease transmission particularly in multihost disease systems.

To our knowledge, this is the first study documenting serological evidence of CDV in invasive minks in South America. The seroprevalence of CDV is similar to that observed in the domestic dog population in the region. Acknowledging the limitations of the use of serology as an indicator of infection (Gilbert et al. 2013), we can conclude



Figure 2. Co-occurrence of American mink and Southern river otters at otter latrine sites. **a** Mink visiting otter latrine (time 0), **b** otter visiting the same latrine depicted in **a** (time interval 2.7 days). **c** Mink visiting an otter latrine (time 0), **d** otter visiting the same latrine depicted in **c** (time interval 1.3 days).

Table 3. Multivariable Logistic Regression Results of Risk Factors Associated with CDV Antibodies in Serum Samples from Owned Dogs ($n = 59$) Using Seroneutralization Test in Chaihuín River, Chile

	Positive	Negative	OR (95% CI)	P value
Location				
Chaihuín	22	22	1	
Cadillal	3	12	0.20 (0.04–0.79)	0.0328
Age				
Adult	21	20	1	
Juvenile	4	14	0.23 (0.05–0.82)	0.0319
Dog roaming				
Restricted	3	5	1	
Unrestricted	22	29	1.39 (0.27–8.12)	0.6911

Goodness of fit for the model was adequate ($P 0.57$).

that CDV is circulating in the ecosystem in both wild and domestic species. This represents a major risk to endangered species that are present in the area such as the river

otter and the recently discovered population of the critically endangered Darwin’s fox (*Lycalopex fulvipes*) (Farías et al. 2014).

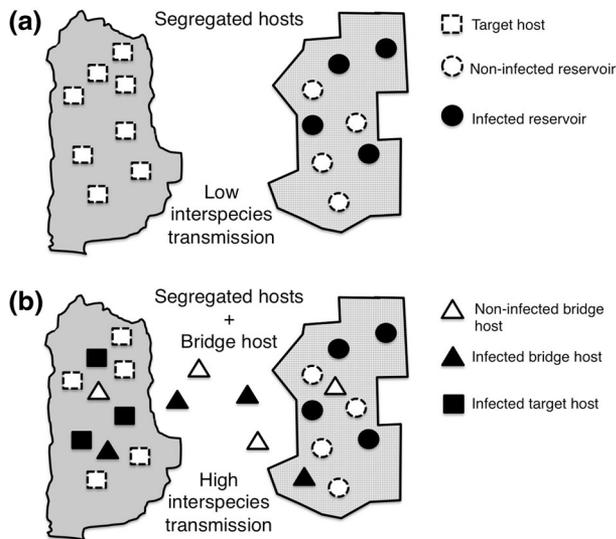


Figure 3. Schematic representation of the “bridge host” concept in a multihost pathogen system. **a** Represents a host community where the target and reservoir host are segregated and therefore there is a low risk of disease transmission. **b** Represents the same host community but adding the invasive “bridge host”. The range of the new host overlaps the ranges of the formerly segregated hosts facilitating disease transmission from the reservoir to the target host.

Although we did not sample otters, the high seroprevalence detected in mink, and the high contact rates between both species, suggest that otters may have also been exposed to this virus. Mustelids, such as the black-footed ferret, are highly sensitive to CDV (Thorne and Williams 1988; Deem et al. 2000) and in Florida, a CDV outbreak affected a threatened population of American mink (*N. vison evergladensis*) (Cunningham et al. 2009). In the case of otters, CDV antibodies have been described in the American river otter (*Lontra canadensis*) (Kimber et al. 2000), and CDV-caused mortality in Eurasian otters (*Lutra lutra*) and Asian clawless otter (*Aonyx cinereus*) has been reported both in captive and wild populations (Geisel 1979; Madsen et al. 1999; Mos et al. 2003; De Bosschere et al. 2005) providing evidence that CDV is an actual threat to otters. In the ecosystem we studied, the only previous accounts of CDV in wild carnivores is a clinical case of CDV in a chilla fox (*Lycalopex griseus*) (Gonzalez-Acuña et al. 2003). In addition, the death of three Darwin’s foxes was likely caused by CDV (Jiménez et al. 2012). In light of this evidence, we suggest that CDV is an important threat for some of the endemic carnivores that inhabit the area.

Considering the conservation status of the Southern river otter (Sepúlveda et al. 2008) and the Darwin’s fox

(Jiménez et al. 2008), we propose a precautionary management of CDV in this ecosystem. Domestic dogs are an important and abundant host reservoir of CDV (Cleveland et al. 2000; Acosta-Jamett et al. 2011; but see Prager et al. 2013), thus, it is important to vaccinate dogs against CDV (Cleveland et al. 2006) and approaches such as vaccination ring campaigns should be given priority. Furthermore, CDV seroprevalence in dogs was lower in the more isolated settlement, suggesting that urban areas are a source of distemper in this region as previously reported (Acosta-Jamett et al. 2011). Controlling the immigration of dogs to the area may be an important strategy in reducing the incidence of CDV. Vaccination of otters and other endangered carnivores is probably not feasible given the difficulties and dangers involved in trapping rare and secretive species. In addition to managing the dogs, we recommend monitoring and controlling mink. Even if contact rates between otters and dogs are low in the study area, mink are likely to facilitate the transmission of CDV between dogs and otters. This, in addition to other known impacts of mink on native fauna (Schüttler et al. 2009; Jiménez et al. 2013), could warrant mink control programs in sensitive areas. Minks could also be used as pathogen sentinels to obtain a better understanding of CDV and other pathogens in this environment. Minks, unlike otters and other native carnivores, have high abundances and are relatively easy to capture and sample compared to native species such as the southern river otter (Sepúlveda et al. 2007, 2011). If campaigns to control mink (e.g., culling) are implemented, managers should be aware of potential consequences since reductions in carnivore densities can disrupt territorial structures resulting in an influx of new individuals and potentially increasing inter-species interactions and disease transmission (Hutchings and White 2000; White et al. 2008).

Overall, our study reveals how an introduced species can alter multihost interactions and in theory act as a bridge host between common domestic species and rare native wildlife. Cross-species behavioral scent marking was a particularly interesting finding that should be further investigated as a means of indirect disease transmission among species. In the future, understanding these kinds of indirect interactions within and between species will be important to better manage disease transmission risk in wildlife and domestic animals. This further emphasizes the importance of understanding the role of behavior in carnivore interactions and their consequences for multihost pathogen dynamics.

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