

Mink (*Neovison vison*) as a natural vector in the dispersal of the diatom *Didymosphenia geminata*

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Considerable resources have been invested worldwide in response to the spread of the diatom *Didymosphenia geminata* in rivers and streams. Considering the very low possibility of elimination of an invasive microbe, management has focused on biosecurity protocols, addressed exclusively toward the human role in dispersal (e.g. ‘check, clean dry’ campaigns and gear-washing stations for recreational users). Natural dispersal by wildlife vectors may also play an important role in the spread of *D. geminata* and other algal species, potentially limiting or negating the efficacy of biosecurity measures. We investigated the possibility that introduced mink (*Neovison vison*) may be a potential dispersal agent for *D. geminata* and other stream diatoms in Chilean Patagonia. *Neovison* were trapped near a zone of strong and persistent *D. geminata* blooms in the fifth order Río Simpson, and also in a fourth order upstream tributary, Río Huemules, the latter with smaller, more incipient blooms. Epibiotic *D. geminata* cells were identified from *Neovison* at Río Simpson (44% positive, average 791 cells per animal, $n = 18$ animals), and Río Huemules (20% positive, average 40 cells per animal, $n = 5$ animals). Many other species were also observed: 20 genera, 5683 cells per mink in Río Simpson, and 18 genera, 3605 cells per mink in Río Huemules. *Navicula*, *Epithemia*, *Fragilaria* and *Placoneis* were among the genera most frequently encountered. *Neovison* are known to prefer the riparian ecotone of streams of all sizes, have the capacity to travel several kilometers upstream and downstream, and possibly as far as 10 km overland to colonize new catchments. Together with an estimated survival time of 60 or more days for *D. geminata* in a humid environment (e.g. mink fur), *Neovison* represent a potentially significant factor in the colonization of upstream reaches and adjacent catchments. We comment on the potential for other wildlife vectors in Patagonia, and respective alternative patterns of short- to long-distance dispersal of diatoms in continental waters. Our results suggest that wildlife vectors should be considered in the management of *D. geminata*, and in the case of *Neovison*, integrative management of multiple invasive species, and a reassessment of conservation priorities may be necessary.

Keywords: diatom dispersal, wildlife vector, secondary spread, epibiotic flora, biosecurity

Introduction

Natural dispersal by wildlife vectors may play a critical role in the spread of invasive species (Orr 2003). This may be especially important in the case of *Didymosphenia geminata* (Lyngb.) M. Schmidt and other algal or microbial organisms, range expansion possibly being more akin to patterns in epidemiology (*sensu* Floder & Kilroy 2009). If true, wildlife vectors may be as important as habitat suitability in determining the probability of occupation of a potential habitat, and may have a potentially significant influence on generalizations based solely on *D. geminata* traits (e.g. Kilroy et al. 2008, Kumar et al. 2008, Floder & Kilroy 2009, Cullis et al. 2012). That is, suitable habitat may remain unoccupied due to vicariance, depending on the suite of dispersal mechanisms, their relative importance and the respective spatial patterns of dispersal. From an applied perspective, given the considerable investment worldwide in managing *D. geminata* in rivers and streams, wildlife

vectors may limit or negate the efficacy of biosecurity measures focused exclusively on the human role in dispersal (e.g. ‘check, clean dry’ campaigns and gear-washing stations). To date, management of *D. geminata* has not considered wildlife vectors (Reid et al. 2012), a key oversight in terms of conservation planning and efforts to contain or exclude *D. geminata*.

Although the first reports of *D. geminata* in South America date to the early 1960s (Asprey et al. 1964), the first documented ‘blooms’ (*sic*: biomass is principally polysaccharide stalk material) were in 2010, on the Río Espolón in Chilean Patagonia. Nuisance blooms under low-nutrient conditions are both a research challenge and the principal cause of concern over impacts to otherwise unimpacted rivers (Sundareshwar et al. 2011, Kilroy & Bothwell 2012). Within three years, *D. geminata* was confirmed from 11 major watersheds in Chile and Argentina (Fig. 1), ranging over 3000 km from the Bío Bío catchment

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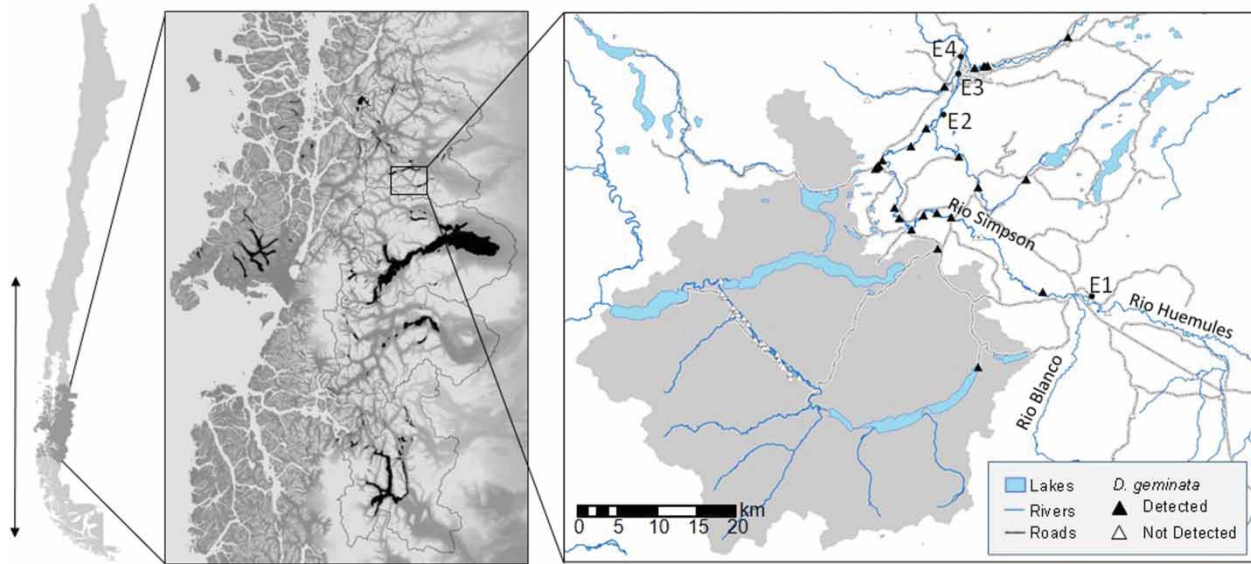


Fig. 1. Map of the study site, Aysén Region, Chile. Scale bar shows the approximate range of *D. geminata* distribution in 2013. Sampling sites on the Río Huemules (E1) and the Simpson at Cinco Rios Lodge (E2), Puente Mundaca (E3) and wastewater treatment plant (E4) are shown. Symbols show locations of previous *D. geminata* surveys (CIEP 2011). The watershed boundary for the Paloma Lakes complex (lower left), which has been prioritized as a *D. geminata*-free zone, is also shown.

(Rivera *et al.* 2013) to the Río Grande in Tierra del Fuego (M. Frangópulos, Centro CEQUA, pers. com.). *Didymosphenia geminata* was presumed to be invasive by government agencies due to a complete lack of recent (post 1960s, see below) observations and the need for a rapid response ('plague' declaration by Subsecretaría de Pesca, Resolución Ex. 2064/2010). Note that Rivera *et al.* (2013) confirmed Asprey's earlier record, but without comment on its native status. Almost all of the recent observations in Chile and Argentina correspond with sites of significant recreational activities, downstream of easy access to rivers (CIEP 2011), access points to lakes (Beamud *et al.* 2013, B. Reid pers. obs.) and population centers. For example, between 2010 and 2011, twelve major rivers within short range of the regional capital Coyhaique (population: 55 000; B. Reid, unpubl. data) were confirmed positive for *D. geminata*. These observations, together with the possible rapid spread over scales of 1000s of kilometers (see above), support its precautionary designation as an invasive organism, and underscore the potential importance of human factors in its range expansion. However, local spread by wildlife vectors may also play a significant role in the dispersal of aquatic organisms (Kristiansen 1996), greatly increasing local secondary spread, and potentially acting synergistically with long-distance human vectors (*sensu* Wilson *et al.* 2008). Potential wildlife vectors in Patagonia include migratory geese (*Chloephaga* spp.) and other aquatic birds, domestic animals, fish (including introduced salmonids) and mink (*Neovison vison*).

Neovison is particularly interesting because of its semi-aquatic habit, possibly facilitating dispersal across terrestrial barriers. Its status as recently introduced and in the

rapid range expansion phase is also important. Given the relative ease of trapping and sampling compared with other potential wildlife vectors, *Neovison* was chosen as the subject of this study. *Neovison* is a carnivorous mammal in the family Mustelidae, whose diet consists principally of aquatic fauna (in Patagonia they are considered a significant predator of native birds). They are highly adapted to swimming, and nearly all of their life cycle is spent in close proximity to lakes and rivers, preferably with some forest cover and moderate slopes in adjacent terrestrial habitats. They are also known to travel significant distances overland, especially during the summer dispersal of young. Native to North America, mink were first introduced to Punta Arenas in southern Chile from 1934 to 1936 for breeding and fur production, and subsequently introduced to the Aysén region on several occasions between 1967 and 1973. Economic problems ultimately led to abandonment and the subsequent liberation of animals, together with undocumented escapes (Jaksik *et al.* 2002, R. Sandoval, Servicio de Agrícola y Ganadero, pers. com.). Naturalized populations of *Neovison* have spread rapidly into most drainage basins, islands and coastal fiords in the region (Cerde 2008). It is formally recognized as 'injurious wildlife' because of potential impacts on the native fauna (Republic of Chile 1996). Based on previous studies, *Neovison* was expected to be abundant along many river reaches known to produce *D. geminata* blooms (J. Cerde, unpubl. data). Moreover, *Neovison* is in its expansion phase in Patagonian ecosystems, hence its dispersal range may be particularly high due to a lack of pressure from conspecifics, together with abundant highly connected habitat.

The potential for wildlife-driven secondary spread (*sensu* Wilson et al. 2008) of *D. geminata* and other aquatic invasives depends on several factors: (1) habitat overlap of the invasive and its dispersal vector, (2) behaviorally mediated contact between wildlife vector and the invader, (3) the dispersal capacity of the wildlife vector, (4) corresponding habitat connectivity allowing for dispersal, and (5) the capacity of the invading species to survive prolonged exposure. In this study, we focus on the first two factors, as applied to the interaction of *D. geminata* and its potential vector, mink (*N. vison*) in southern Chile. The presence of *D. geminata* cells on mink would offer additional evidence of a shared habitat, and that direct contact between the two organisms would not be a limiting factor in the secondary spread of *D. geminata*. Our primary objective was to determine the presence and relative abundance of *D. geminata* on the fur of *Neovison*, as an indicator of the potential for wildlife vectors in the spread of this invasive diatom. We further comment on the interaction between the two introduced species, and how timing of *D. geminata* blooms and *Neovison* life history might variously enhance or inhibit secondary spread. We also comment on the potential for other wildlife vectors in the region, including introduced salmonids and native waterfowl.

Methods

Study area

The fourth order Río Huemules originates from the cold Patagonian cold steppe (Fig. 1), with limited topographic relief, meandering to constrained reaches, and October snowmelt peak (Dirección General de Aguas 2004). Station E1 (Villa El Blanco: 45°48'32.88" S, 71°55'6.60" W) is located near the confluence with the Río Blanco, a cordilleran stream with early December peak flow. The fifth order Río Simpson begins downstream of the confluence, with a mixed regime of pampas and cordilleran hydrology. Stations E2 (Lodge Cinco Rios: 45°36'25.43" S, 72°5'55.70" W), E3 (Puente Mundaca: 45°35'17.60" S, 72°5'2.56" W) and E4 (upstream from a wastewater treatment plant: 45°33'28.52" S, 72°4'29.50" W) occur below the transition from braided channels of medium gravel, to more constrained reaches with steeper valley walls, larger substratum and increased riparian forest cover. Study reaches were selected based on the presence of *D. geminata* blooms (CIEP 2011) and the potential for *Neovison* habitat (J. Cerda, pers. obs.).

Field sampling

Sampling periods were between 31 October and 19 December 2012 for station E1 on the Río Huemules, and between 25 January and 19 February 2013 for stations E2–E4 on the Río Simpson. Sampling was conducted in two distinct phases for each station: field reconnaissance and trapping

of *Neovison* was conducted first (7 and 27 trapping days for Ríos Huemules and Simpson, respectively), followed by sampling of the river benthos (one day each at stations E1 and E2). This was a necessary precaution to avoid cross-contamination between samples from mink and river benthos, which could result in false positives from mink samples (all work in phase one was therefore restricted to the terrestrial environment). Transects were ~ 300 m in length, established roughly parallel to and within 100 m of the river. Up to seven baited Tomahawk-style traps were located in microhabitats considered suitable for *Neovison* (sites with rock outcrops or forest cover, and also based on visual cues, such as tracks and other signs). Site selection was conducted with wildlife professionals from the regional agricultural agency, habitat criteria were based on extensive trapping and sterilization efforts in 2007 (Cerdeña 2008). Captured animals were anesthetized, and brought to the laboratory for epibiotic flora sampling.

Benthic sampling for diatom community composition was carried out following the protocol for *D. geminata* surveys (CIEP 2011). In summary, three stones were selected at random from each of two longitudinal transects parallel to the shore, at depths of 20 and 50 cm to compensate for fluctuations in water level (CIEP 2011), stones were spaced ~ 10 m apart along respective transects (six stones total). Attached algae were dislodged from the entire stone surface with a toothbrush, followed by washing of the stones and brushes with filtered water into double Ziploc bags, and preservation with Lugol's solution. Biosecurity procedures, including the disinfection of field equipment and the use of disposable sampling materials, were used to avoid cross-contamination of samples (CIEP 2011).

Laboratory processing

Consistent with the field sampling, laboratory sampling was executed in two phases to avoid cross-contamination between mink (with expected low cell density) and benthic samples (high cell density from large areas). Cells were harvested from the fur, feet and tails of mink using a toothbrush, *Neovison* and brushes were subsequently washed into disposable Ziploc bags, as described above. Samples were concentrated into 50 mL vials by centrifugation. To avoid cross-contamination, all sampling and handling materials were disposed of between sampling events. Ten-milliliter subsamples were analyzed for cell density following sedimentation (Utermohl chamber). Counts were conducted at ×100 using a Zeiss Axiovert 40C with camera, based on 9–50 photographed fields per sample (depending on sediment interference, generally 5–20 total cells per sample). For analysis of community composition, a series of wet mounts were prepared from 50 µL subsamples of untreated material. An Olympus CX 31 was used, scanning at ×100 along the transects until a minimum total of 50 viable individuals (i.e. with chloroplasts) were encountered, identifying to the

level of genus at $\times 400$. Confirmation of identification at the generic level was conducted at the Museo de la Plata, Argentina, based on material treated to eliminate organic matter, following the method described in CEN/TC 230 (2002). Samples were mounted in Naphrax®, and analyzed DM 2500 at $\times 400$, equipped with a Leica DFC420 camera. Krammer & Lange-Bertalot (1986, 1988, 1991a, 1991b), Rumrich *et al.* (2000), Schoeman & Archibald (1980), and Simonsen (1987) were used for identification. Nomenclature follows Fourtanier & Kociolek (2011).

Data processing

Total cell density on *Neovison* was calculated based on subsample volume and the calibrated field of view of photographs (Villafañe & Reid 1995). Epibiotic species density per animal was based on analysis of the community

composition and total density. Basic statistical characterization (mean and standard deviation) was calculated using Microsoft Excel.

Results and discussion

Epibiotic flora of *Neovison*

Live cells of *D. geminata* were positively confirmed for 20% of *Neovison* captured at the Río Huemules ($n = 5$) and 44% of animals sampled at the Río Simpson ($n = 18$). Evidence of mink tracks on exposed *D. geminata* mats (Fig. 2) indicated that contact with the water is not necessarily a prerequisite for contact between diatoms and wildlife vectors. *Didymosphenia geminata* cell density on *Neovison* averaged 40 and 791 cells per animal for the Huemules and Simpson rivers, respectively (Table 1). Total diatom

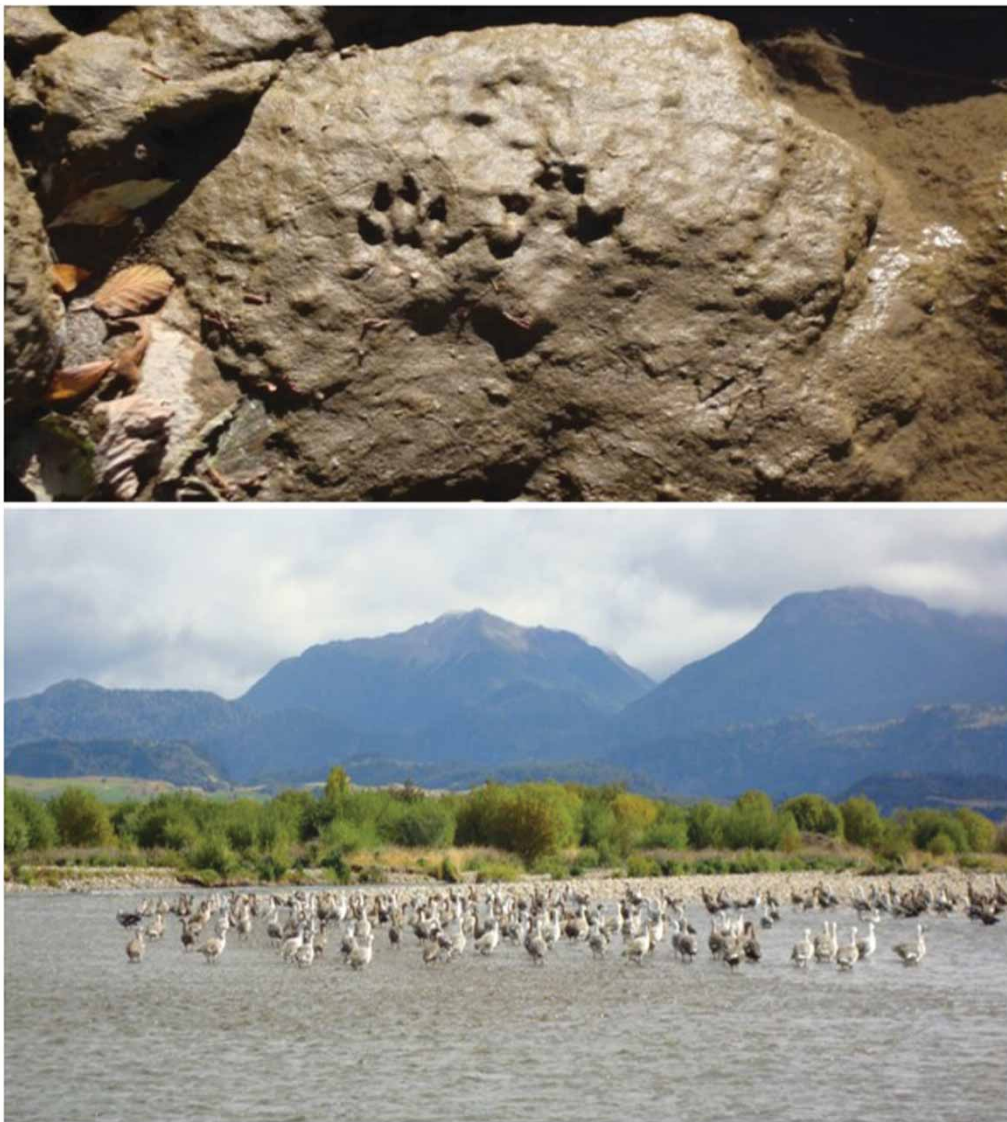


Fig. 2. Evidence for wildlife vectors for *D. geminata*: photo of mink tracks on *D. geminata* mat (upper) and migratory Patagonian geese (*Chloephaga picta*, *C. poliocephala*) resting in an area of *D. geminata* blooms in the Río Simpson (lower).

Table 1. Presence and abundance of *D. geminata* and other epibiotic diatoms on *Neovison*.

	Huemules		Simpson	
Number of mink sampled	5		18	
Cell density (number/mink)	3605 (± 1620)		5683 (± 2847)	
Density of <i>D. geminata</i>	45 (0–225)		791 (0–2330)	
Frequency of <i>D. geminata</i>	0.20		0.61	
	Mink	benthos	mink	Benthos
Total taxa	18	15	20	10
% <i>D. geminata</i>	1.8 (0–6.7)	7.7	12.9 (0–50.0)	11.7
Dominant taxa	<i>Navicula</i>	<i>Navicula</i>	<i>Navicula</i>	<i>Navicula</i>
	<i>Epithemia</i> , <i>Fragilaria</i> , <i>Placoneis</i>	<i>Epithemia</i>	<i>Didymosphenia</i>	<i>Cocconeis</i>
	<i>Pinnularia</i>	<i>Cocconeis</i>	<i>Epithemia</i>	<i>Epithemia</i>

Note: Values in parentheses indicate range, with the exception of values for cell density which are standard deviation.

Table 2. Summary of epibiotic diatom flora on *Neovison vison*: frequency of occurrence on trapped *Neovison* individuals at Río Huemules ($n = 5$) and Río Simpson ($n = 18$).

	Río Huemules				Río Simpson			
	Frequency (%)	Density (number/mink)	Mink (% taxa)	Benthos (% taxa)	Frequency (%)	Density (number/mink)	Mink (% taxa)	Benthos (% taxa)
<i>Aulacoseira</i>	0.00	0.0	0.0	0.0	0.33	86.9 (± 164)	1.5	0.0
centrales	0.40	125.9 (± 172)	2.7	0.0	0.33	85.4 (± 147)	1.8	0.0
<i>Cocconeis</i>	0.60	98.3 (± 113)	3.7	14.69	0.33	49.5 (± 93)	1.2	27.3
<i>Cymbella</i>	0.80	182.6 (± 141)	5.5	2.80	0.78	360.8 (± 351)	6.0	0.0
<i>Cymatopleura</i>	0.00	0.0	0.0	1.40	0.39	85.4 (± 129)	2.0	0.0
<i>Didymosphenia</i>	0.20	45.1 (± 101)	1.8	7.69	0.61	791.0 (± 857)	12.9	11.7
<i>Diploneis</i>	0.20	7.5 (± 17)	0.3	0.0	0.00	0.0	0.0	0.0
<i>Epithemia</i>	1.00	409.3 (± 101)	11.9	17.48	0.94	768.1 (± 806)	12.2	15.6
<i>Fragilaria</i>	0.80	338.6 (± 210)	11.9	2.10	0.44	225.8 (± 373)	3.6	2.6
<i>Frustulia</i>	0.80	124.3 (± 80)	4.3	1.40	0.61	217.0 (± 350)	3.5	0.0
<i>Gomphoneis</i>	0.60	92.4 (± 103)	3.7	6.29	0.89	455.0 (± 364)	8.5	9.1
<i>Gomphonema</i>	0.80	175.5 (± 179)	5.2	4.20	0.56	126.6 (± 136)	3.3	3.9
<i>Hannaea</i>	0.40	34.7 (± 51)	1.2	0.0	0.00	0.0	0.0	0.0
<i>Melosira</i>	0.60	80.0 (± 109)	2.4	1.40	0.5	181.1 (± 298)	2.9	0.0
<i>Navicula</i>	1.00	621.7 (± 435)	15.5	22.38	1.00	1212.8 (± 909)	22.2	28.6
<i>Nitzschia</i>	0.20	14.1 (± 31)	0.6	2.80	0.61	122.2 (± 113)	2.9	0.0
<i>Pinnularia</i>	0.60	400.8 (± 489)	11.9	4.20	0.22	369.1 (± 386)	1.0	6.5
<i>Placoneis</i>	0.80	677.1 (± 1154)	9.4	0.0	0.67	40.2 (± 86)	6.3	0.0
<i>Rhopalodia</i>	0.00	0.0	0.0	0.0	0.17	18.5 (± 44)	0.4	0.0
<i>Staurosira</i>	0.00	0.0	0.0	0.0	0.06	15.0 (± 63)	0.6	0.0
<i>Surirella</i>	0.80	213.8 (± 299)	6.4	8.39	0.67	326.7 (± 450)	5.5	10.4
<i>Synedra</i>	0.60	63.2 (± 102)	1.8	2.80	0.22	145.9 (± 356)	1.6	2.6

Note: Also shown is the estimated density (\pm SD) of respective genera encountered on *Neovison*, and % community composition for animal and corresponding benthic flora.

density was 3605 (± 1620) cells from 18 genera, and 5683 (± 2847) cells from 20 genera, respectively. For both sites, the dominant epibiotic genus was *Navicula*, followed by *Epithemia*, *Fragilaria* and *Placoneis* for Río Huemules, and *Didymosphenia* for Río Simpson (Table 2). The epibiotic flora was generally similar to the corresponding benthos. Limited cell counts and under-representation of the home range of respective animals probably renders any comparison of community composition between corresponding animal and benthic populations difficult.

Neovison as a potential dispersal vector for *D. geminata*

Our results confirm that *Neovison* is a possible vector for *D. geminata* secondary spread. It would be difficult, if not impossible, to demonstrate that *D. geminata* cells on *Neovison* fur can successfully colonize new unoccupied habitat. However the semi-aquatic nature of *Neovison*, combined with the high resistance of *D. geminata* cells to desiccation, suggest that, over medium to longer time scales, the probabilities are likely significant. The *Neovison* daily range is ~ 1 km along stream corridors, but, more importantly, it is

not restricted to downstream movement only (downstream dispersal of *D. geminata* is probably controlled by physical movement through flowing water). Where population densities are low, *Neovison* may have much higher dispersal ranges of 5–9 km (i.e. rate of range expansion in Argentina, Fasola *et al.* 2011). The colonization of Argentina from Chile required crossing mountain passes over 1000 m in elevation (Jaksik *et al.* 2002), demonstrating the potential of both *Neovison* and their attached algae to spread across adjacent high-elevation catchments. Finally, *Neovison* may clearly be a dispersal vector for other benthic diatoms, a natural example of mass dispersal (*sensu* Wilson *et al.* 2008). The selectivity of taxa is currently unknown, although it appears that certain taxa were either under-represented (*Cocconeis*, *Epithemia*) or over-represented (*Surirella*, *Navicula*, *Pinnularia*) on *Neovison* pelt. Low cell counts prohibit statistical treatment of the data. We note that the probability of attached algal colonization via wildlife dispersal vectors may depend on the desiccation resistance of the algal taxa and the host microenvironment (e.g. humid pelt).

Although the results clearly demonstrate the physical overlap of habitats, temporal factors also present an additional consideration: how does the phenology of *D. geminata* blooms (or more importantly the timing of peak cell density) compare with the life history and activity patterns of *Neovison*? If consistent with the northern hemisphere, the life history of *Neovison* is characterized by juvenile dispersal in mid-summer, and a decreased home range in winter (Gerell 1970). Meanwhile, *D. geminata* blooms generally appear to follow the snowmelt peak, blooming in October–December in rivers originating in the pampas (Río Huemules) and in December–March for streams with cordilleran snowmelt influence (Río Simpson). One might speculate that there is greater synchronization of algae and host in mid-summer in cordilleran stream ecosystems.

Other potential *D. geminata* vectors in Patagonia

Epibiotic algae, including diatoms, have been documented from marine hosts (e.g. substratum, but also suggesting dispersal potential) ranging from ciliates to whales (Tiffany 2011). The phenomenon is much less studied in continental waters. One noteworthy exception is in Cladocera (Allen & De Stasio 1993, Pérez-Martínez *et al.* 2001), where extreme diatom densities, > 100 000 *Synedra* cells per individual cladoceran (Allen & De Stasio 1993), and potential synchronization of *Korshikoviella* zoospore production with *Daphnia* molt. Evidence for the colonization of more mobile vertebrate organisms in continental waters by epibiotic algae is limited to turtles (Wetzel *et al.* 2011). Although there is abundant evidence for algae associated with marine cetaceans (Holmes 1985, Holmes *et al.* 1993, Denys 1997), there are limited studies on epibiotic diatoms on fish. *Cladophora* on rainbow trout is a rare example

(Dodds & Gudder 1992), the holdfasts being anchored to bone, not the scales.

Mucus, a protective and aerodynamic coating common to salmonids, has an unknown effect on colonization by diatoms or other algal epibionts. Preliminary sampling by scraping, removing scales and mucus of rainbow trout (*Onchoryhincus clarkii*), has so far revealed no diatoms on over 20 specimens (P. Bus, unpubl. data). Rainbow trout are known to have relatively well-developed mucus compared with other salmonids (Fast *et al.* 2001). One might speculate that Chinook (*Onchoryhincus tshawytscha*), established and expanding its range in many Patagonian catchments (Ibarra *et al.* 2011), may be a more favorable vector due to its physical deterioration during the periods leading up to spawning, and to the high level of contact with shallow substrata in headwaters. Spawning by Chinook in late March and early April in Patagonia may correspond with the observed pattern in *D. geminata* in the Río Huemules: sparse upstream *D. geminata* populations concentrated in shallow riffles in April 2011 led to the original speculation that salmonids are potential *D. geminata* dispersal vectors (B. Reid, pers. obs.). We know of no viable methods for sampling large salmonids without increasing contact with the substratum, which would contaminate the sample. New upstream introductions observed in subsequent phases of *D. geminata* spread on the South Island of New Zealand (Kilroy & Unwin 2011) may be the result of fish or other wildlife vectors. If certain fish function as dispersal vectors for algae, the introduced trout and salmon populations (Pascual *et al.* 2007), which are some of the most significant global invaders (Cambrey 2003), offer the potential for colonizing microbes to take advantage of these successful invaders.

Waterfowl are well-known vectors for aquatic organism dispersal (Kristiansen 1996), particularly jump dispersal (*sensu* Wilson *et al.* 2008), enabling longer distance dispersal across watersheds. Direct contact between native geese and *D. geminata* populations has also been observed at our study site (Fig. 2) and on the Río Baker (Reid *et al.* 2012). The latter is possibly the largest continuous *D. geminata* population in South America (Reid & Torres 2013) and a major stopover for waterfowl migration. Such invasion pathways depend on migration routes, primarily north–south along the southern Andes for Patagonian geese (*Chloephaga* spp.), but also with significant east–west migration to and from wintering areas in coastal northern Patagonia (Canevari 1996).

Management implications

Our results suggest that wildlife vectors should be considered in the management of *D. geminata*. In the case of *Neovison*, management of multiple invasives (integrated management of aquatic ecosystems) or a reassessment of conservation priorities (which sites, if any, can be

defended), may be necessary. Fig. 1 illustrates one potential example, adapted from Reid et al. (2012). Isolated reaches in the Paloma Lakes complex, identified as having both economic/conservation value and being potentially defensible due to their hydrographic isolation, are the only sites (as of 2013) near the regional capital where the presence of *D. geminata* has not yet been confirmed. Determination of *Neovison* movement corridors, modeling of potential habitat, and consideration of possible control programs and the relative costs and benefits of such actions may be necessary for the conservation of this area. As argued previously (Reid et al. 2012), the considerable investment in monitoring a single invasive organism, and biosecurity programs at the regional and national level aimed solely at the human elements, may ultimately be of limited success in the long term.

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