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Contamination of an arctic terrestrial food web with marine-derived persistent organic pollutants transported by breeding seabirds

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This study provides evidence of contaminant transport by seabirds to a coastal Arctic food web.

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ABSTRACT

At Cape Vera, Devon Island (Nunavut, Canada), a colony of northern fulmars (*Fulmarus glacialis*) concentrates and releases contaminants through their guano to the environment. We determined whether persistent organic pollutants (POPs) from seabirds were transferred to coastal food webs. Snow buntings (*Plectrophenax nivalis*) were the most contaminated species, with ∑PCB and ∑DDT (mean: 168, 106 ng/g ww) concentrations surpassing environmental guidelines for protecting wildlife. When examined collectively, PCB congeners and DDT in jewel lichen (*Xanthoria elegans*) were lower in samples taken farther from the seabird colony, and increased with increasing $\delta^{15}N$ values. However, only concentrations of p'p-DDE:∑DDT and PCB-95 were significantly correlated inversely with distance from the seabird cliffs. Linkages between marine-derived POPs and their concentrations in terrestrial mammals were less clear. Our study provides novel contaminant data for these species and supports biovector transport as a source of organic contaminants to certain components of the terrestrial food web.

1. Introduction

Despite strict restrictions on the production and usage of some persistent contaminants and pesticides across North America and Europe, contaminant concentrations remain high in the fauna and indigenous populations of the Arctic (AMAP, 2004). The air–plant–animal pathway is the main route for persistent organic pollutants (POPs) such as polychlorinated biphenyls (PCBs) and organochlorines (OCs) entering Arctic terrestrial food webs, as illustrated in studies of the lichen → reindeer → wolf food chain (Thomas et al., 1992, AMAP, 1998, Kelly and Gobas, 2001). However, the transfer of contaminants by migratory species (biovector transport), may also be an important pathway of contaminant entry to food webs (e.g., Evenset et al., 2004; Blais et al., 2005, 2007). Biotransport will bring contaminants to sites where they can enter the local food chain through regular mechanisms (e.g. via lichens), and is not as such a different pathway into the terrestrial food web. Biovector transport is accomplished by predators or high order consumers; therefore, their contaminants have already undergone food web biomagnification prior to their transfer to the receptor food web (Blais et al., 2007).

At Cape Vera, Devon Island, Nunavut (Fig. 1), a seabird colony of ~10,000 breeding pairs of northern fulmars (*Fulmarus glacialis*) concentrate and release contaminants through their guano to the coastal ecosystem (Blais et al., 2005; Michelutti et al., 2009). For example, hexachlorobenzene, dichlorodiphenyltrichloroethane (DDT), and total mercury (THg) concentrations in surface sediments from ponds located close to the bird cliffs were 10×, 60×, and 20× higher, respectively, than in sediment from ponds more distant from the seabird colony (Blais et al., 2005). In our companion study (Choy et al., 2010), we found significantly higher values of nitrogen stable isotopes ($\delta^{15}N$) in food webs adjacent to the Cape Vera colony compared to samples collected farther from the colony, or at a distant reference site, which collectively demonstrated a gradient of seabird influence on marine-derived nutrients entering the terrestrial food web. Somewhat surprisingly, we did not record a corresponding enrichment effect between proximity to the seabird colony and total mercury (THg) concentrations in biota.

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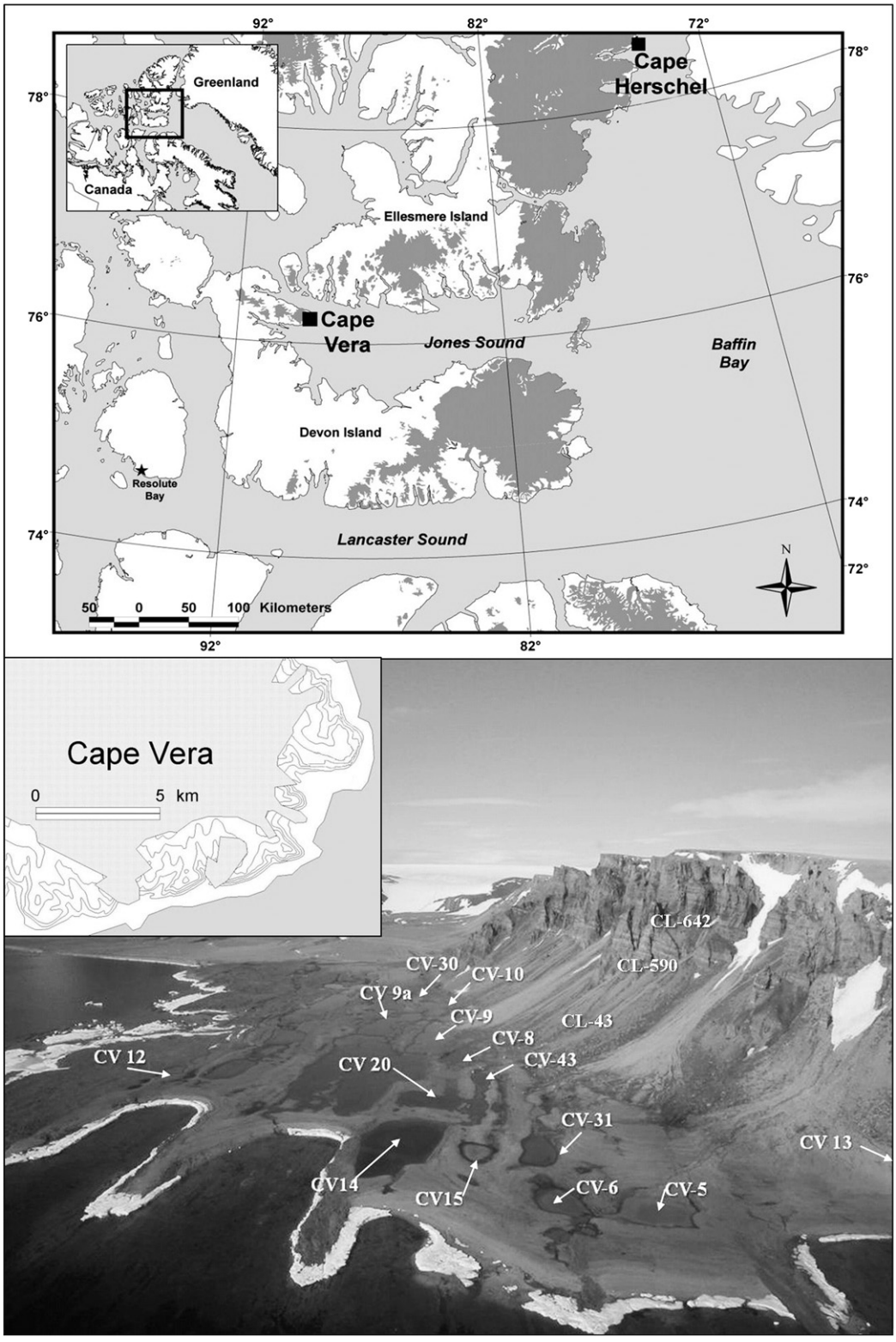

Fig. 1. Main study site at Cape Vera, Devon Island, Nunavut (76°15′ N, 89°15′W) and our reference site at Cape Herschel, Ellesmere Island, Nunavut (78°37′ N, 74°42′W) (Douglas and Smol, 1994). Arrows and labels indicate ponds where samples were collected at the base of the seabird cliffs. Photograph taken by John Smol in 2004. Modified from Choy et al., (2010).

In this paper, our objective was to determine whether lipophilic POPs were being transferred to organisms in the coastal food webs at Cape Vera. As top predators and scavengers in the marine food web (Mallory, 2006), northern fulmars biomagnify POPs (AMAP, 1998; Fisk et al., 2001). In seabirds, contaminant patterns from their prey are reflected in guano (Evenset et al., 2004). Consequently, we expected that the deposition of guano along the cliffs, which contributes contaminants to nearby ponds, would result in

higher POP concentrations in organisms closest to the colony compared to unaffected reference sites, in contrast to our findings on Hg (Choy et al., 2010).

We examined polychlorinated biphenyl (PCB) and DDT concentrations in selected food web components at Cape Vera and made comparisons to those gathered from Arctic areas without seabird colonies. Contaminants were measured in five species: jewel lichen (*Xanthoria elegans*), worm lichen (*Thamnolia vermicularis*), northern collared lemming (*Dicrostonyx groenlandicus*), snow bunting (*Plectrophenax nivalis*) and ermine (*Mustela erminea arctica*). These five species are elements of the local terrestrial ecosystem, and we assessed trophic linkages in this web using $\delta^{15}N$. The ermine is a top predator at Cape Vera and preys on both insectivorous buntings and herbivorous lemmings. Jewel lichen is an ornithogenic lichen found near bird roosts (Brodo et al., 2001). Cape Vera is distant from any sources of direct contamination with the exception of the large seabird colony, so local fauna should have elevated contaminant levels relative to other parts of the Arctic if fulmar guano is enhancing coastal contamination. Moreover, relationships between distance from the seabird colony or $\delta^{15}N$ with contaminant concentrations in lichens would only be expected if biovector transport was the main source of contamination.

Only trace amounts of DDT-related compounds have been measured in Arctic air masses (Barrie et al., 1992; Su et al., 2008). Thus, in Arctic sites where DDT concentrations in organisms are relatively high, the source of that DDT is unlikely to be solely atmospheric. The ratio of DDT to its metabolites, such as *p'p*-DDT/*p'p*-DDE and $\sum$DDT/$\sum$DDE, can help determine if contaminants were processed by the marine food web, rather than derived strictly from atmospheric sources (Roosens et al., 2007). It has been found that *p'p*-DDE forms 98.7–100% of $\sum$DDT in the guano of little auk (*Alle alle*), kittiwake (*Rissa tridactyla*), and glaucous gulls (*Larus hyperboreus*); (Evenset et al., 2004). *p'p*-DDE, a DDT metabolite with a high biomagnification potential, concentrates in top predators and comprised ~86% of $\sum$DDT in northern fulmars (Buckman et al., 2004). At Cape Vera, the concentrations of all DDTs were very low (collectively, they comprised less than 1% of total OC pesticides) four XAD resin-based passive air samplers measuring average gaseous air concentrations over a one year period during two consecutive years (2006 and 2007) at three locations away from and at the base of the seabird colony (K. Foster, pers. comm.); however, DDE/DDT in pond sediment increased with proximity to the seabird cliffs (Blais et al., 2007). Therefore, the relative proportion of DDE/DDT will help identify if seabird input is the main source of DDT contamination to food webs.

We predicted that concentrations of PCBs in lichens, particularly congeners common in fulmars (PCB-153, 180, 138, 99, 118), would be higher in samples collected closer to the seabird colony. Lichens typically acquire airborne contaminants; thus more volatile, lower chlorinated PCB congeners (PCB-66/95, 70, 101, and 52) are typically most abundant in Arctic lichens (AMAP, 1998). We also analyzed lower-chlorinated PCB congeners (PCB-18, 31–28, 44, 49, 52, 87, 101) that are typically eliminated by seabirds (Elliott, 2005) to see if our predicted relationships were unique to biomagnifying congeners. Although we were unable to associate THg in vegetation with seabird influence (Choy et al., 2010), PCBs are strictly anthropogenic and, therefore, inputs from guano will not be confounded with natural sources.

2. Methods

2.1. Study area

Cape Vera (Fig. 1; 76°15′ N, 89°15′W) is located on Devon Island, Nunavut. Cliffs used by breeding birds extend 6.4 km along the coastline and are 245–313 m above sea level (Gaston et al., 2006). We sampled a series of 12 sites adjacent to ponds (CV5, 6, 8, 9, 9a, 10, 13–15, 20, 30, 31) located below the seabird cliffs with distances between ponds and the cliffs spanning 4 km (Blais et al., 2005).

Samples of lichen were collected at different elevations and from rocky ledges at the base of the seabird cliff. Jewel lichens were collected on the cliffs at elevations of 119 m (CL590) and 140 m (CL 642) above sea level and along a rocky ledge 6 m high at the base of the cliff (CL 43), next to CV43 approximately 34 m from the main cliff inhabited by nesting fulmars.

Reference ponds (CV1 and 12) were located 2.5–4 km away from the immediate influence of the seabird colony (Fig. 1). Lichens were also collected near ponds ($n = 3$) at coastal Cape Herschel, Ellesmere Island (Fig. 1; 78°37′N, 74°42′W), an area without colonial nesting seabirds.

2.2. Sample collection and preparation

All food web samples were collected between 1–20 July 2006 and 8–21 July 2007. Jewel and worm lichens were collected in 50 mL falcon tubes that were pre-rinsed with acetone and hexane. Three falcon tubes of each lichen species were collected near the 13 ponds in 2006. In 2007, samples of worm and jewel lichen were taken from varying altitudes along the seabird cliff and at reference sites CV1 and Cape Herschel. Jewel lichens were carefully scraped off of flat rocks using field knives that were cleaned and dried between pond sites. Worm lichens were collected using stub-ended tweezers. Samples were put on sea ice in a cooler until they were transferred to the freezer room at the Polar Continental Shelf Program (PCSP) base at Resolute Bay, Nunavut.

Several small animals were collected from Cape Vera. Fifty Victor® snap traps were set in 2006 and 2007 beside burrows of *Dicrostonyx groenlandicus*, the northern collared lemming, and checked every morning and evening. Weight and sex of the five captured lemmings were recorded.

We captured 18 snow buntings in 2006 and in 2007 using Victor® traps or by shooting with a 12 gauge shot gun using steel pellets. All buntings were sexed and sealed in freezer bags. In 2007, five buntings were captured from CV1 as controls. In 2007, two ermine were captured. All animal samples were removed from snap traps using nitrile gloves, placed in bags, and labelled with the GPS coordinate or closest pond and were put on sea ice in a cooler until they were transferred to a freezer.

At the University of Ottawa, animal samples were dissected and prepared for POP and stable isotope analysis. Mammals were weighed, sexed, and skinned: the gastrointestinal tract was removed. Birds were weighed, and plucked of feathers; the gastrointestinal tract was removed for stomach content analysis. Animal samples were homogenized using liquid nitrogen in the M20 IKA Works® Universal Mill. After homogenization, 1–2 g subsamples were placed in microcentrifuge tubes for stable isotope analysis. The mill was cleaned with distilled water and ethanol and dried in between samples. All samples were freeze-dried for 72 h and re-homogenized.

2.3. Stable isotope analyses

Freeze-dried whole body tissue was used for stable isotope analyses after running a preliminary test between different tissues which showed that the stable isotope values for liver were the same as for whole body in lemmings, ermine, and buntings. Samples were analyzed for $\delta^{15}N$ at the G.G. Hatch Isotope Laboratory at the University of Ottawa using well-established and standard procedures (Peterson and Fry, 1987). Samples were flash combusted at 1800 °C in an elemental analyser (EA) (EA 1110, CE Instruments, Italy) coupled to a stable isotope mass spectrometer (DeltaPlus Advantage IRMS, ThermoFinnigan, Germany) with a Conflo interface (Conflo III). Nitrogen stable isotope values were calculated relative to atmospheric nitrogen (N_2) with an analytical precision of $\pm 0.2‰$. Triplicate assays were run every sixth sample.

2.4. Contaminant and lipid analysis

Methods for PCB and DDT analysis followed the National Laboratory for Environmental Testing (NLET) protocol (Environment Canada, Burlington, ON, Canada). Whole body tissues (8 g wet weight [ww]) were homogenized in Hydromatrix® (Varian, Harbour City, CA, USA) and packed into 33 mL cells for the accelerated solvent extractor (ASE200, Dionex, SunnyvaleCA, USA). A set of recovery surrogates was added to each sample (Ultra Scientific, North Kingston, RI, USA).

The samples were extracted in the ASE200 with methylene chloride (Omnisolv®, Fisher Scientific, Ottawa, ON, Canada). Lipid removal was completed using a preparative liquid-chromatograph (Agilent Technologies, Mississauga, ON, Canada). Fractionation and instrument performance was determined by repeated injections of a GPC Calibration Standard containing corn oil and methoxychlor (CLP-340, Ultra Scientific, North Kingston, RI, USA).

A chromatographic column was packed with 8 g of activated silica gel (Davisil 635, Fisher Scientific, Mississauga, ON, Canada) in hexane for the final clean-up. Non-polar OCs and PCBs were eluted using 50 mL of hexane, followed by 80 mL of 1:1 hexane:methylene chloride to elute polar OCs. Samples were evaporated down to 500 μl in iso-octane and 2.5 pg of octachloronaphthalene (Ultra Scientific) was added as an internal standard. To determine lipid content, 1 g of whole body tissue was extracted using methylene chloride. The extraction was left to evaporate, oven dried, and lipid weight was determined gravimetrically.

PCBs and OCs were determined using an Agilent 6890 gas chromatograph with a ^{63}Ni micro electron-capture detector (Agilent Technologies). A 1 μL extract was injected, using a splitless injection, with an inlet temperature of 280 °C and constant flow of helium at 33 cm/s on a 60 m × 250 μm × 0.25 μm DB-5MS capillary column (Agilent Technologies). Chromatograms were screened for 39 PCB congeners and DDT. The quantification of ∑PCB was the total of PCB congeners 5, 8, 14, 18, 19, 28, 29, 31, 44, 49, 52, 66, 87, 99, 101, 105, 110, 118, 128, 132, 138, 149, 153, 155, 156, 157, 163, 170, 180, 183, 187, 194, 195, 200, 203, 206, 209. ∑DDT was the total of four congeners (*p'p*-DDE, *p'p*-DDD, *p'p*-DDT, *o'p*-DDT).

Recovery and blank corrections were made on each sample. Surrogate standards were used to determine the recoveries of the analyzed compounds. Mussel Standard Reference Material 2978 (National Institute of Standards and Technology, Gaithersburg, MD, USA) was run routinely with sample batches. Using approximately 0.25 g (dw), the average recovery for the Standard Reference Material® 2978 for 22 PCB congeners was 72 ± 25% SD ($n = 6$) and for five pesticides 65 ± 31% SD ($n = 5$). Coefficients of variation for ∑PCB duplicates in samples were low (range 0.5–11%), as were those for OCs (range 4–13%). Procedures for determining method detection limits (DL) followed standard protocols identified by Gouin et al. (2005). Values below DL were given values of DL/2 as per Baccarelli et al. (2005).

2.5. Statistical analysis

All data were analyzed using Systat® 12, SigmaPlot® 10 (Systat Software, Point Richmond, CA, USA), and Canonical Community Ordination (CANOCO) software 4.5 (Biometris, Wageningen, the Netherlands). Analysis of covariance (ANCOVA), *t*-tests, and linear regressions were performed using Systat®12.

Many compounds were below detection limits in worm lichen. Lichens vary in their response to pollutants, restricting the utility of some species to monitor contaminant levels (Rossbach and Lambrecht, 2006). We are unaware of any prior, published study that has used worm lichen to measure POPs, whereas jewel lichen has been used to monitor spatial patterns of trace element and organohalogen concentrations (Matschullat et al., 1999). Because of difficulties in the extraction process (i.e., low sample weight) of POPs in worm lichen, we focused statistical analyses on jewel lichen.

Regression analyses were run on lower-chlorinated PCBs (PCB-18, 28–31, 44, 49, 52, 87 and 101) and biomagnifying PCBs (PCB-99, 118, 138–163, 153, 170, 180, 194, and 195) ∑PCB, ∑DDT, and DDE:∑DDT ratio. PCBs that were not detected in lichen samples (PCB 5–8, 14, 19) or were only measured in one sample (PCB-29, 66) were not included in the statistical analyses. Transformations were performed on data until acceptable levels of normality and constant variance were achieved. We did not apply sequential Bonferroni corrections to *p*-values, as our results came from planned comparisons, and they satisfied reasonable and logical expectations (Moran, 2003). We used ANCOVA to test for relationships between PCBs or OCs and δ^{15}N, with % lipid in the sample as a covariate (Hebert and Keenleyside, 1995). Principal components analyses of the PCB congener concentrations in jewel lichen were performed using CANOCO® 4.5.

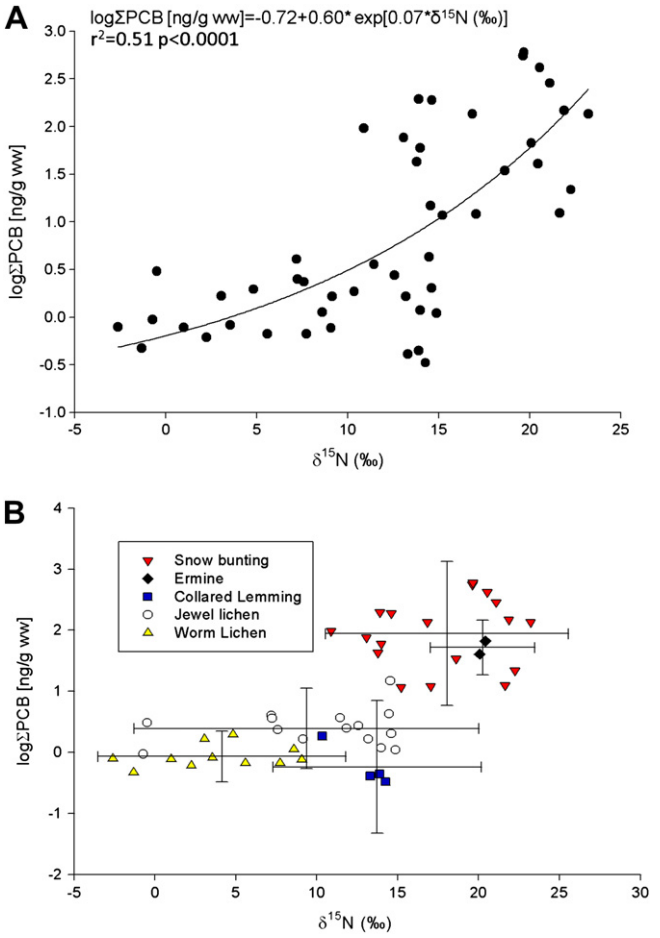

Fig. 2. The non-linear relationship (f = y0 + a*exp(b*x)) between log ∑PCB [ng/g ww] and δ^{15}N values among members of the ecosystem at Cape Vera, Devon Island, Nunavut. Errors bars represent the 95% confidence intervals surrounding the means of log ∑PCB [ng/g ww] and δ^{15}N for each species.

3. Results and discussion

3.1. Contaminants in the Cape Vera ecosystem

Across all organisms that we sampled, those feeding at higher trophic levels (e.g., higher δ^{15}N) had higher ∑PCB [ng/g ww] ($r^2_{49} = 0.51$, $p < 0.001$) and higher ∑DDT [ng/g ww] concentrations ($r^2_{49} = 0.54$, $p < 0.001$; Figs. 2 and 3). The relationships remained significant when contaminants were lipid-normalized. However, no relationships were significant within individual species (Fig. 3).

Snow buntings were the most contaminated organisms at Cape Vera by lipid and wet weight, followed by ermine, lichen, and lemmings (Table 1, Figs. 2 and 3). Buntings feed primarily on chironomids whose larval stages are aquatic (Falconer et al., 2008). The sediment-chironomid pathway is a main route for PCB contamination to tree swallows (*Tachycineta bicolor*), with 94% of PCB concentrations in nestlings accumulated through diet (Maul et al., 2006). Mean ∑DDT concentrations in snow buntings and ermine (Table 1) surpassed Canadian (14 ng/g ww), and exceeded or were near U.S. Environmental Protection Agency (USEPA; 39 ng/g ww) environmental quality guidelines for the protection of wildlife (Braune et al., 1999). Mean ∑PCB concentrations in snow buntings also exceeded USEPA guidelines of 160 ng/g (ww) and International Joint Commission guidelines for the protection of aquatic life and wildlife (100 ng/g ww; Braune et al., 1999). The ∑PCB concentrations tended to be higher in adults (ANOVA, $F_{2,15} = 2.9$, $p = 0.09$), but both hatch year ($n = 9$) and adult buntings ($n = 9$) had concentrations above contaminant guidelines. Levels of ∑DDT were lower in hatch year buntings than in adult females (ANOVA, $F_{2,14} = 4.3$, $p = 0.04$; Tukey test, $p = 0.04$). Buntings from Cape Vera had up to eight times higher ∑PCB concentrations than buntings from Greenland and Rankin Inlet (Burnham and Mattox, 1984; Court et al., 1990; Johnstone et al., 1996).

Since snow buntings are seasonal migrants, it is unclear how much of their contaminant burden is from Cape Vera compared to their winter grounds. Snow buntings from most Arctic regions migrate from southern Ontario and the United States, but the buntings at Cape Vera arrive very early in the year, and may migrate from Greenland (Falconer et al., 2008). Buntings are herbivores during the winter (Lyon and Montgomerie, 1995), and it seems unlikely that seeds in differing winter locations could contribute to the very large differences in PCB and DDT (Table 2), particularly given that Cape Vera buntings feed on chironomids from ponds with high POPs (Blais et al., 2005). Future analysis on POP concentrations in chironomids, the main prey of snow buntings at Cape Vera, will establish if buntings receive their contaminants from Cape Vera or their winter grounds.

As a top predator, one might initially expect ermine to have the highest contaminant concentrations. Although they consume buntings, their main prey is lemmings (Gilg et al., 2006), which represent 98.5% of their scat in winter. As a year-round inhabitant of

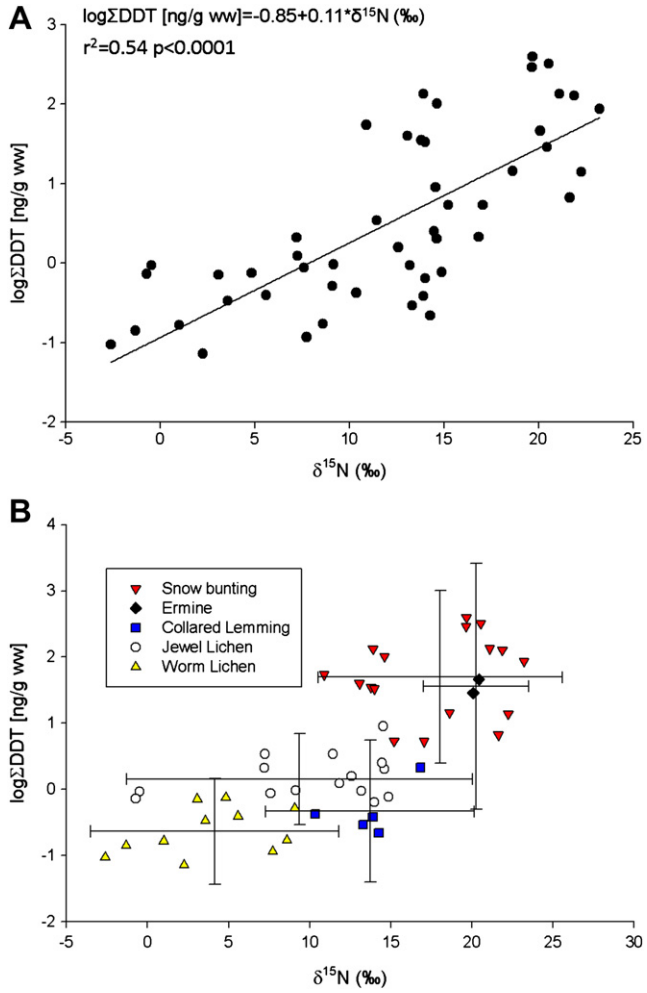

Fig. 3. A. The relationship between log ∑DDT [ng/g ww] and δ^{15}N values among members of the ecosystem at Cape Vera, Devon Island, Nunavut. B. Errors bars represent the 95% confidence intervals surrounding the species means of log ∑DDT [ng/g ww] and δ^{15}N values for each species.

Cape Vera, ermine probably accrue most of their POPs from lemmings, but they feed on snow buntings (notably young in nests) during the summer. Ermine have the ability to metabolize congeners that have no chlorine substitutions (below) which may have contributed to lower contaminant concentrations than buntings (Leonards et al., 1998). However, our ermine results may also be influenced by low sample size. Ermine at Cape Vera had 60- to 170-fold higher levels of ∑PCB and ∑DDT than lemmings (Table 1). There are few contaminant data for ermine, but ∑DDT (<1 ng/g) and ∑PCB (13.7 ng/g) concentrations in ermine muscle from Grande Baleine, Québec (AMAP, 1998) were both lower than values at Cape Vera (SOMER Inc. 1993a,b).

Table 1
Summary of mean and standard errors of stable isotope and contaminant data for organisms collected from Cape Vera. δ^{15}N values were provided from Choy et al. (2010).

Species	N	% Lipid	δ^{15}N (‰)	∑DDT [ng/g ww]	∑PCB [ng/g ww]	PCB-153 [ng/g ww]
Worm Lichen	11	4.19	4.14 ± 0.88	0.31 ± 0.07	0.94 ± 0.14	0.12 ± 0.03
Jewel Lichen	14	1.69	9.37 ± 1.19	2.04 ± 0.60	3.28 ± 0.93	0.54 ± 0.21
Collared Lemming	5	2.36	13.7 ± 1.04	0.71 ± 0.32	0.76 ± 0.37	0.11 ± 0.07
Snow Bunting	18	2.91	18.1 ± 0.73	105.9 ± 29.2	168 ± 43.1	63.9 ± 16.8
Ermine	2	6.5	20.3 ± 0.18	37.3 ± 8.72	53.8 ± 12.9	18.4 ± 5.44

Many of the PCB congeners and DDT concentrations in lemmings were less than or at detection limits. Nonetheless, ∑DDT and ∑PCB concentrations in lemmings from Cape Vera were much higher than lemmings from Rankin Inlet (Table 2; Johnstone et al., 1996). Jewel and worm lichen collected at CL43 had the highest level of ∑PCB and ∑DDT of all lichen samples (Tables S1, S2). Similarly, CL43 had the highest concentrations of THg in jewel lichen, purple saxifrage, and tufted saxifrage (Choy et al., 2010).

3.2. Biomagnifying congeners and metabolites in relation to seabird influence

Biomagnifying PCBs (PCB-153, 118, 138/163, 180, and 99) were dominant congeners in snow buntings and ermine (Fig. 4). Ermine and other mustelids can metabolize congeners that lack chlorine substitutions in the *meta* and *para*-position, as well as PCB-101 and 149 (Leonards et al., 1998). Collared lemmings also had high proportions of PCB-153, 138/163, and 180, but had more variation in their congener profiles (Fig. 4). Lichen expressed variable congener profiles, which were not dominated by lower chlorinated compounds (PCB-66/95, 52, 101), in contrast to other Arctic studies of lichen (AMAP, 1998). In order of decreasing contributions, the most abundant congeners found in jewel and worm lichen at Cape Vera were PCB-153, 138/163, 180 and 118, each comprising 4.4–14.1% of ∑PCB.

In jewel lichen, all measured PCB congeners, as well as DDT and its derivatives, were lower in samples taken farther from the seabird colony (12 regressions, all $r > 0.1$; binomial test, $p = 0.0002$). However, only the regressions for *p'p*-DDE:∑DDT ($r^2 = 0.37$, $p = 0.046$) and PCB-95 ($r^2 = 0.31$, $p = 0.048$) showed a statistically significant decline in contaminant concentrations with increasing distance from the seabird colony. Similarly, in all 12 comparisons using jewel lichen, highly chlorinated congeners tended to be positively correlated with increasing δ^{15}N values (binomial test, $p = 0.0002$), but only the relationship with log PCB-138/163 was statistically significant ($r^2 = 0.39$, $p = 0.01$).

Lower chlorinated PCBs in jewel lichen showed no statistically significant pattern with distance from the seabird colony (all $p > 0.05$). Unlike the results for higher chlorinated PCBs, eight of nine lower chlorinated congeners were lower in lichen samples with higher δ^{15}N values (binomial test, $p = 0.018$), with statistically significant correlations for PCB-18 ($r^2 = 0.33$, $p = 0.02$), PCB-31–28 ($r^2 = 0.32$, $p = 0.03$), and PCB-44 ($r^2 = 0.38$, $p = 0.01$).

A principal components analysis (PCA) of PCB congener data normalized to PCB-153 (to create a relative index of biomagnification) was performed to discern how specific congeners partitioned in jewel lichen collected from sites of varying contamination (Fig. 5). The first axis explained 80.1% of the total variance whereas the second axis explained 11.3%, for a combined total of 91.4%. Lichens collected from Cape Herschel were separated from those collected at Cape Vera, indicating different sources of contamination. Lichens collected near pond CV9, with very low concentrations of PCBs, were also isolated from the other lichens (Fig. 5). Most of the samples from Cape Vera were clustered together, indicating similar congener patterns. There were differences among lichens collected from cliffs and CV10, CV8, and CV20, which had a greater contribution of higher chlorinated PCBs (Fig. 5). Similarly, congeners PCB-153, 138, 118, and 180 were the main constituents of fulmar guano, while PCB-18, 31–28, and 49 on average composed 40% of the ∑PCB of gaseous concentrations in air (K. Foster, pers. comm.).

Table 2
Mean contaminant whole body data for lemmings and snow buntings from Cape Vera and other regions of the Arctic.

Species	Location	Year	N	∑DDT [ng/g ww]	DDE [ng/g ww]	DDE range [ng/g]	DDE [lipid wt]	∑PCB [ng/g ww]	∑PCB range [ng/g ww]	∑PCB [lipid wt]	Study
Collared Lemming	Cape Vera	2006	5	0.69	0.105	ND-0.27	–	0.76	0.33–1.86		This study
Collared Lemming[a]	Rankin Inlet	1993–94	13	ND	ND	–	–	ND		–	(Johnstone et al., 1996)
Snow Bunting	Cape Vera	2006–07	18	106	98.4	4.3–380	4802	168.0	11.7–601	8225	This study
Snow Bunting	Rankin Inlet	1993–94	2	–	NO	0–70	–	ND		–	(Johnstone et al., 1996)
Snow Buntings	Rankin Inlet	1982–83	5	ND	ND	–	–	ND	–	–	(Court et al., 1990)
Snow Buntings	West Greenland-inland survey	1973	1	–	80	–	1900	NO	–	–	(Burnham and Mattox, 1984)
Snow Buntings	West Greenland-inland survey	1979	4	–	80	32–110	1640	20	18–30	470	(Burnham and Mattox, 1984)
Snow Bunting	Coastal East Greenland	1973	2	–	70	60–70	1700	NO	–	ND	(Burnham and Mattox, 1984)

ND means calculated mean is below detection limit (PCBs: 0.1 ng/g, DDT: 0.02 ng/g Johnstone et al., 1996). Sample concentrations for snow buntings from Court et al. (1990) were labelled "not detected" but no detection limit was provided. NO means no analytical response.
[a] Only 1 lemmings had detectable contaminant levels (∑PCB of 4.17 ng/g, DDE = 0.11, DDD = 0.70, and DDT = 0.80 ng/g).

4. Conclusions and future directions

In our previous study (Choy et al., 2010), we found that THg concentrations in coastal food webs at Cape Vera were not significantly enriched relative to other Arctic sites. In contrast, in our current study, three lines of evidence support our hypothesis that biotransport of contaminants by fulmars has enriched contaminant levels in the local food web near the seabird colony.

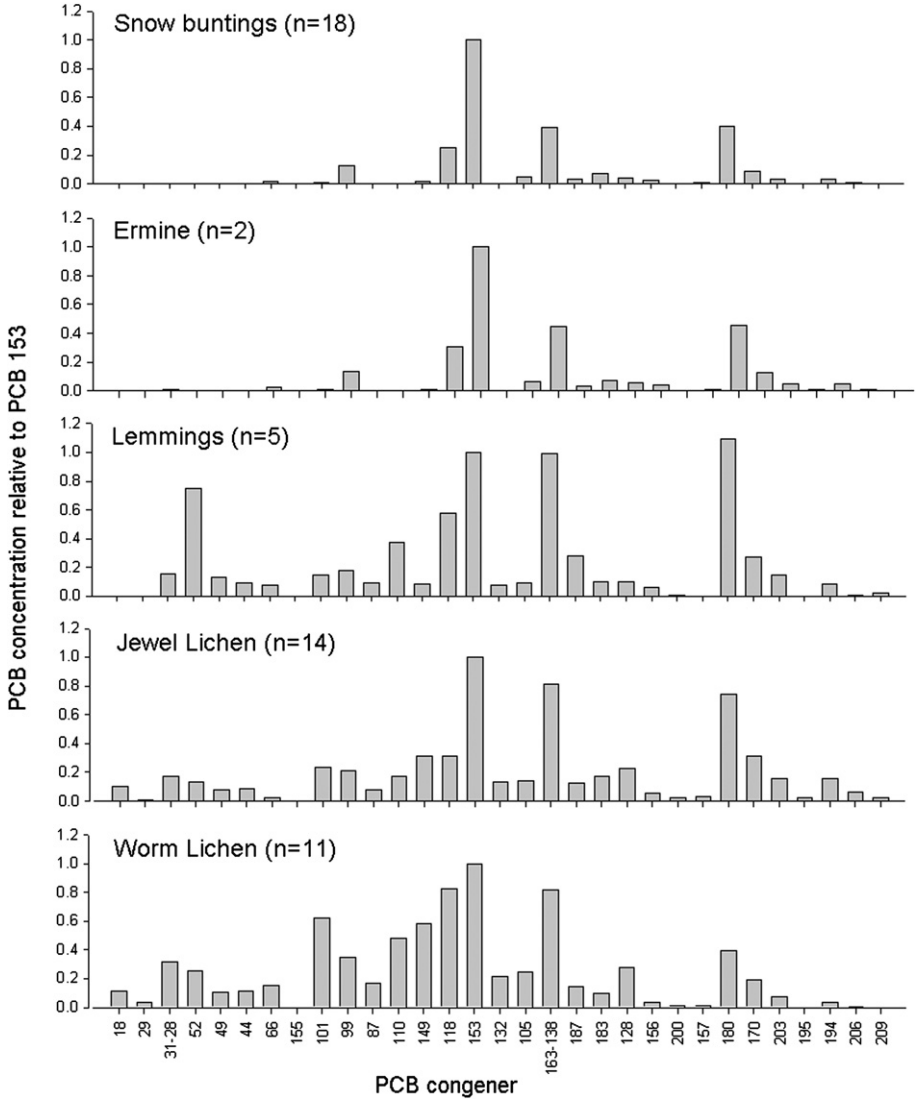

Fig. 4. Mean PCB congener concentrations normalized to PCB-153 for each species collected from the Cape Vera food web (2006–2007).

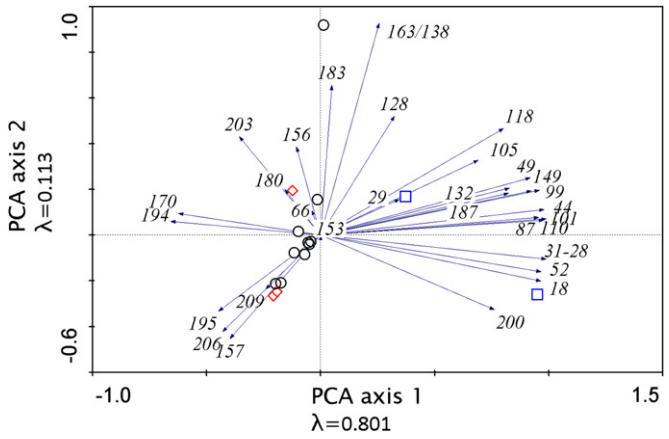

Fig. 5. PCA biplot of PCB congeners normalized to PCB-153 in jewel lichen from 15 sites at Cape Herschel and Cape Vera. Numbers represent different congeners (e.g., 200 refers to CB-200). Lichens collected near reference ponds at Cape Herschel are represented by squares, near affected ponds at Cape Vera by circles and on cliffs by diamonds.

First, concentrations of POPs in snow buntings at Cape Vera were higher than values reported elsewhere (Table 2), often exceeding environmental quality guidelines. Second, jewel lichen samples taken farther from the seabird cliffs had lower concentrations of POPs than those adjacent to the seabird colony. Although most of our regressions of POP concentrations in jewel lichen were not statistically significant (possibly due to small sample sizes), all of the tests had positive correlations with indicators of seabirds influence (12 regressions, all $r > 0.1$; binomial test, $p = 0.0002$; i.e., higher POP concentrations in lichens collected in areas of greater seabird influence). Third, there was a relatively higher enrichment of biomagnifying POPs in jewel and worm lichen collected close to the seabird colony, as would be expected if seabird inputs were the source of contamination to the system. In this and our previous study (Choy et al., 2010), we found that vegetation collected from the ledge had the highest contaminant concentrations, suggesting it may be a heavily contaminated site.

To our knowledge, this is the first study to provide data on PCB and OC concentrations in jewel lichen, worm lichen, and ermine in the Canadian Arctic, and the first to report concentrations in any of these species from the High Arctic. In addition, we expect that other coastal food webs may also experience contamination if situated near a seabird colony, and this should be considered in assessments of ecological risk of contaminants. While our results are specific to Cape Vera, the process of biotransport of contaminants by seabirds is truly global (e.g., Evenset et al., 2004; Blais et al., 2007; Roosens et al., 2007).

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Appendix. Supplementary material

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.envpol.2010.07.014.

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