Ecography

Supplementary material

Electronic Supplementary Materials

This file contains additional information on Methods and Results for

Linking genetic and ecological differentiation in an ungulate with a circumpolar distribution

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Appendix 1

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Table A1 Sampling sites and number of individuals (*N*=1297) for caribou and reindeer (*Rangifer tarandus*) herds and ecotypes across the species' Holarctic distribution. All individuals were genotyped at 16 nuclear microsatellites (see Material and Methods).

	Herd	Province/State	Country	Abr.	lat	long	*N*	Ecotype	Size (*Nc*)	Years	Source
1	Kangerlussuaq-Sisimiut	Greenland	Greenland	KaSi	67.08	-50.90	29	Migratory tundra	98300	2010	CARMA (2016)
2	Svalbard	Svalbard	Norway	Sval	78.11	15.41	20	Svalbard	1720	2005	Reimers et al. (2011)
3	Finnmark *	Norway	Norway	FinK	70.00	25.10	24	Domestic	182500	2013	Johnsen et al. (2015)
4	Varanger *	Norway	Norway	Vara	70.37	30.00	12	Domestic	10000	2011	Henden et al. (2011)
5	Hardangervidda	Langfjella	Norway	Harda	60.10	7.03	14	Migratory tundra	6000	2002	CARMA (2016)
6	Iceland *	Eastern Iceland	Iceland	Icel	65.09	-15.07	27	Introduced	4800	2013–2014	Russell and Gunn (2013)
7	Snøhetta	Rondane Dovre	Norway	Snoh	62.30	9.20	24	Migratory tundra	2000	2000-2011	Jordhøy et al. (2012)
8	Finland	Finland	Finland	Finl	64.40	29.30	23	Boreal forest	960	2007	MAF (2007)
9	Wrangel *	Chukotka	Russia	Wran	71.25	-179.67	6	Introduced	500	2007	Sheremetev et al. (2014)
10	Nenetsky *	Nenetsky	Russia	Nenet	68.32	53.16	7	Domestic	100000	2000	Taras Sipko Pers. Comm
11	Yamal *	Yamalia	Russia	Yaml	69.96	70.09	3	Domestic	380000	2012	Golovatin et al. (2012)
12	Taymyr	Taymir	Russia	Taym	71.55	90.08	61	Migratory tundra	750000	2003	CARMA (2016)
13	Lena	Yakutia	Russia	Lena	72.77	123.76	36	Migratory tundra	95000	2009	CARMA (2016)
14	Western Arctic	Alaska	USA	WesA	67.52	-158.30	25	Migratory tundra	235000	2013	CARMA (2016)
15	Northern Alaska Peninsula	Alaska	USA	NoAP	57.56	-156.95	20	Mountain	2000	2011	Mager et al. (2014)
16	Teshekpuk	Alaska	USA	Tesh	69.21	-154.79	20	Migratory tundra	32000	2013	CARMA (2016)
17	Denali	Alaska	USA	Dena	63.33	-150.50	6	Mountain	2100	2011	Mager et al. (2014)
18	Central Arctic	Alaska	USA	CenA	70.02	-148.95	22	Migratory tundra	70000	2013	CARMA (2016)

19	White Mountains	Alaska	USA	WhiM	65.53	-147.59	20	Mountain	650	2011	Mager et al. (2014)
20	Porcupine	Yukon	Canada	Porc	67.67	-141.04	29	Migratory tundra	197000	2013	CARMA (2016)
21	Tay River	Yukon	Canada	TayR	62.15	-132.35	7	Mountain	3750	1996	Hegel and Russell (2013)
22	South Nahanni	Yukon	Canada	SNah	62.18	-128.59	22	Mountain	2100	2009	Hegel and Russell (2013)
23	Bluenose East	Northwest Territories	Canada	BluE	66.13	-117.85	31	Migratory tundra	68000	2013	CARMA (2016)
24	Bathurst	Northwest Territories	Canada	Bath	64.44	-112.42	28	Migratory tundra	35000	2012	CARMA (2016)
25	Ahiak/Beverly	Nunavut	Canada	AhBv	63.26	-104.44	50	Migratory tundra	195000	2011	CARMA (2016)
26	Qamanirjuaq	Nunavut	Canada	Qama	60.52	-97.94	22	Migratory tundra	345000	2008	CARMA (2016)
27	Dolphin-Union	Nunavut	Canada	DoUn	69.55	-109.36	14	Migratory tundra	30000	2012	Serrouya et al. (2012)
28	Bathurst Island	Nunavut	Canada	Peary	75.77	-99.78	20	Peary	187	2012	Serrouya et al. (2012)
29	Columbia-North	British Columbia	Canada	ColN	51.66	-118.63	24	Mountain	155	2012	Serrouya et al. (2012)
30	A La Peche	British Columbia	Canada	ALPe	53.54	-118.79	20	Mountain	135	2013	Weckworth et al. (2013)
31	Narraway	British Columbia	Canada	Narr	54.39	-120.30	20	Mountain	100	2013	Weckworth et al. (2013)
32	Besa Prophet	British Columbia	Canada	BePr	57.47	-123.37	21	Mountain	100	2012	Environment Canada (2012)
33	Cold Lake	Alberta	Canada	CoLa	54.46	-110.18	20	Boreal forest	125	2012	Serrouya et al. (2012)
34	RedEarth	Alberta	Canada	RedE	57.10	-114.70	20	Boreal forest	275	2012	Serrouya et al. (2012)
35	Caribou Mountain	Alberta	Canada	CarM	59.19	-115.59	20	Boreal forest	350	2012	Environment Canada (2012
36	Chinchaga	Alberta	Canada	Chin	57.51	-119.01	20	Boreal forest	250	2012	Environment Canada (2012
37	Naosap Lake	Manitoba	Canada	NaoL	54.86	-101.40	23	Boreal forest	200	2012	Environment Canada (2012
38	The Bog	Manitoba	Canada	TBog	53.35	-101.18	8	Boreal forest	75	2012	Environment Canada (2012
39	Harding Lake	Manitoba	Canada	HarL	56.11	-98.22	20	Boreal forest	125	2012	Environment Canada (2012
40	Charron Lake	Manitoba	Canada	CharL	53.00	-95.78	19	Boreal forest	500	2012	Environment Canada (2012
41	Val d'Or	Quebec	Canada	VaOr	47.74	-78.21	25	Boreal forest	20	2012	Équipe de rétablissement du caribou forestier du Québec (2013)

42	La Sarre	Quebec	Canada	LaSa	48.77	-79.17	30	Boreal forest	492	2012	Environment Canada (2012
43	Temiscami	Quebec	Canada	Temi	50.57	-75.48	26	Boreal forest	110	2002	Équipe de rétablissement du caribou forestier du Québec (2013)
44	Port-Neuf	Quebec	Canada	PoNe	49.13	-70.41	35	Boreal forest	50	2004	Équipe de rétablissement du caribou forestier du Québec (2013)
45	Pipmuacan	Quebec	Canada	Pipm	49.66	-70.27	29	Boreal forest	134	2012	Environment Canada (2012
46	Manicouagan	Quebec	Canada	Manic	50.96	-68.53	34	Boreal forest	181	2012	Environment Canada (2012
47	Bowater	Quebec	Canada	Bowa	50.45	-71.75	33	Boreal forest	480	2007	Équipe de rétablissement du caribou forestier du Québec (2013)
48	La Romaine	Quebec	Canada	Roma	50.98	-63.36	31	Boreal forest	240	2009	Équipe de rétablissement du caribou forestier du Québec (2013)
49	Lac Joseph	Labrador	Canada	LJos	52.45	-64.65	37	Boreal forest	1047	2009	(Schmelzer 2011)
50	RedWine	Labrador	Canada	Rwin	53.21	-61.63	20	Boreal forest	97	2012	Environment Canada (2012
51	Mealy Mountain	Labrador	Canada	Mealy	53.67	-57.68	14	Boreal forest	1604	2012	Environment Canada (2012
52	Rivière-George	Quebec	Canada	Geor	55.72	-63.99	25	Migratory tundra	14200	2014	CARMA (2016)
53	Torngat	Labrador	Canada	Torn	58.24	-63.22	23	Mountain	930	2014	Couturier and Mitchell Foley (2014)
54	Rivière-aux-Feuilles	Quebec	Canada	Leaf	56.89	-73.95	25	Migratory tundra	430000	2011	CARMA (2016)
55	Gaspésie	Quebec	Canada	Gasp	48.93	-66.28	29	Mountain	103	2012	Lalonde and Michaud (2013)
56	Gaff Topsails	Newfoundland	Canada	GaTop	49.15	-56.65	13	Boreal forest	2800	2010	Morrison et al. (2012)
57	Pot Hill	Newfoundland	Canada	PHill	48.59	-55.72	11	Boreal forest	4200	2010	Morrison et al. (2012)

*: indicate semi-domestic or introduced populations.

3- Description of environmental variables

Table A2 Description of the variables used to estimate environmental distances among the studied populations of caribou and reindeer (*Rangifer tarandus*) across the species' Holarctic distribution.

	Variable	Description	
Veg.	NPP	Net primary productivity	[1-km] [1]
	TREE	Proportion of tree cover	[8-km] [2]
Temp.	BIO1	Annual Mean Temperature	[1-km] [3]
	BIO2	Mean Diurnal Range (Mean of monthly [max temp - min temp])	[1-km] [3]
	BIO3	Isothermality (BIO2/BIO7) (* 100)	[1-km] [3]
	BIO4	Temperature Seasonality (standard deviation *100)	[1-km] [3]
	BIO5	Max Temperature of Warmest Month	[1-km] [3]
	BIO6	Min Temperature of Coldest Month	[1-km] [3]
	BIO7	Temperature Annual Range (BIO5-BIO6)	[1-km] [3]
	BIO8	Mean Temperature of Wettest Quarter	[1-km] [3]
	BIO9	Mean Temperature of Driest Quarter	[1-km] [3]
	BIO10	Mean Temperature of Warmest Quarter	[1-km] [3]
	BIO11	Mean Temperature of Coldest Quarter	[1-km] [3]
Precip.	BIO12	Annual Precipitation	[1-km] [3]
	BIO13	Precipitation of Wettest Month	[1-km] [3]
	BIO14	Precipitation of Driest Month	[1-km] [3]
	BIO15	Precipitation Seasonality (Coefficient of Variation)	[1-km] [3]
	BIO16	Precipitation of Wettest Quarter	[1-km] [3]
	BIO17	Precipitation of Driest Quarter	[1-km] [3]
	BIO18	Precipitation of Warmest Quarter	[1-km] [3]
	BIO19	Precipitation of Coldest Quarter	[1-km] [3]
Elev.	alt	Digital elevation model	[1-km] [3]

[1] MODIS satellite images (Kucharik et al. 2000)
[2] http://www.landcover.org (DeFries et al. 2000)
[3] WorldClim Version 1.4 (Hijmans et al. 2005)

4- Additional information on genetic differentiation

Genetic distances between pairs of populations were initially estimated as F_{ST} according to Weir and Cockerham (1984), Cavalli-Sforza chord distance Dc (Cavalli-Sforza and Edwards 1967), G''_{ST}, a standardized measure of population differentiation based on Nei's G_{ST} (Hedrick 2005, Meirmans and Hedrick. 2011), and Jost's D, a metric that is independent of the amount of genetic diversity within samples (Jost 2008). F_{ST}, Cavalli-Sforza chord distance Dc, G''_{ST}, and Jost's D were computed using GENODIVE 2.0b27 (Meirmans and Van Tienderen 2004). Because Cavalli-Sforza chord distance Dc, G''_{ST}, and Jost's D distances were highly correlated (all Pearson's correlations $r > 0.96$; Fig. A1), we only used F_{ST} and Dc distances for further analyses.
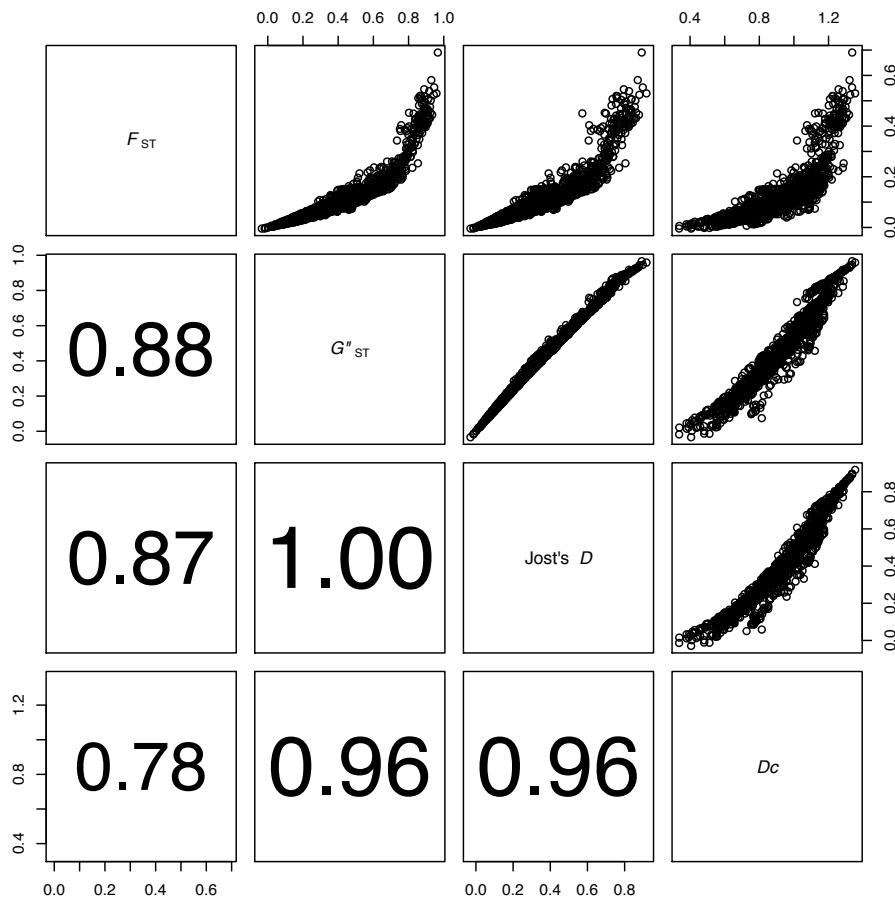

Figure A1 Pearson's correlation among genetic distances between pairs of populations

The degree of genetic differentiation (F_{ST}) among herds ranged between 0.00 and 0.69 (mean F_{ST} = 0.11, 95% CI 0.10:0.12) within the Euro-Beringian lineage and between 0.00 and 0.24 (mean F_{ST} = 0.08, 95% CI 0.07:0.09) within the North American genetic lineage. Within the Euro-Beringian lineage, the herds from Greenland and Svalbard displayed the highest levels of genetic differentiation both between them (F_{ST} = 0.69, $P <$ 0.001) and in comparison with other herds (average F_{ST} Greenland = 0.44±0.07, 95% CI 0.42: 0.46; average F_{ST} Svalbard = 0.41±0.06, 95% CI 0.40: 0.43). Within the North American lineage, the highest levels of genetic differentiation were found between the herds from Newfoundland and the herds from the mainland (mean F_{ST} = 0.14, 95% CI 0.12:0.15) and with isolated herds (*e.g.*, average F_{ST} Gaspésie = 0.19±0.06, 95% CI 0.17: 0.20). Semi-domestic herds from Russia also displayed significant levels of genetic differentiation with the closest natural populations (see Fig. 3), probably due to low sample sizes or bottlenecks and loss of neutral genetic diversity by strong drift during domestication. Chord distances (*Dc*) across all populations ranged from 0.00 to 1.35 (mean *Dc* = 0.92, 95% CI 0.90:0.93), from 0.00 to 1.34 within the Euro-Beringian lineage (mean *Dc* = 0.87, 95% CI 0.85:0.89), and from 0.00 to 1.06 within the North American lineage (mean *Dc* = 0.64, 95% CI 0.60:0.68).

5- Harmonic mean of census population sizes among fictitious pairs of populations
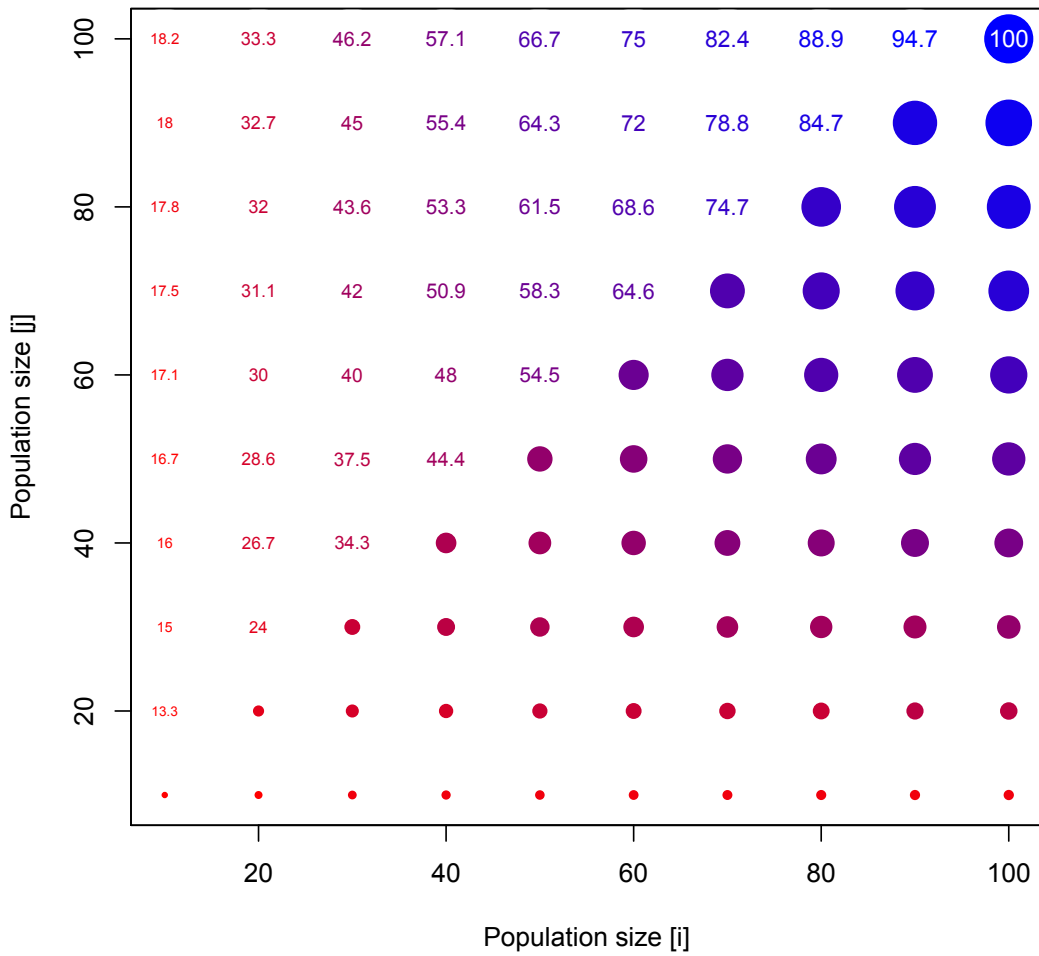

Figure A2 Harmonic mean of census population sizes (*Nc*) among fictitious pairs of populations *i* and *j*. Population sizes range from 10 to 100. *Nc* decrease disproportionally with decreasing population sizes.

6- Statistical analyses

A variety of statistical and analytical methods exists for analyzing distance matrices in landscape genetics (Hanks and Hooten 2013, McCullagh 2009) and have been subject to intensive discussion in the recent literature (Balkenhol et al. 2009, Guillot and Rousset 2013, Jaquiéry et al. 2011, Legendre and Fortin 2010). Here, in addition to the Information Theoretic approach (Burnham and Anderson 2002), we used the "Multiple Matrix Regression with Randomization" function (MMRR; Wang 2013) implemented in R version 3.2.3 (R Development Core Team 2016). MMRR analyses have some of the limitations of Mantel tests (Graves et al. 2013, Guillot and Rousset 2013, Jaquiéry et al. 2011, Legendre and Fortin 2010) but allow incorporating simultaneously multiple predictor distance matrices and estimating their relative effect sizes (Wang 2013). MMRR uses $n \times n$ distance matrices, returns the coefficients of regression and the coefficient of determination (R^2), performs randomized permutations, and estimates significance for all parameters (Wang 2013). MMRRs included genetic distances as response variables and a set of dissimilarity matrices as explanatory variables.

7- Inferring seawater resistance surface

Resistance models can be employed under a wide variety of scenarios, from hypothetical landscapes consisting on binary habitat classes (e.g. habitat/non-habitat) to complex landscapes considering multiple habitat features each with different effects on gene flow (McRae 2006, McRae and Beier 2007). Here, we used a landmass/seawater map reflecting seawater resistance to caribou movement as a more realistic alternative to classical IBD (sse McRae and Beier 2007 for a similar approach). Based on a digital elevation model available from Worldclim version 1.4 with a 1-km resolution (Table A2; Hijmans et al. 2005), we built hypothetical resistance surfaces by setting the value of areas covered by seawater an increasing resistance of 2, 4, 8, 16, 32, 64, 128, 256, 512, and 1024 per raster cell, while

keeping landmass raster resistance costs at 1 (see Schwartz et al. 2009 for a similar

approach). However, while caribou can swim across open water over short distances of 3–10

km (Leblond et al. 2016, Miller 1995, Poole et al. 2010), their movements on sea ice can

reach 380 km (Miller et al. 2005). Therefore, following Geffen et al. (2007) and Jenkins et

al. (2016), we also weighted the landscape resistance for the occurrence of sea ice among

sampling locations. To do so, we retrieved monthly Arctic sea ice extent from 1979 to 2010

available at the National Snow and Ice Data Centre (University of Colorado, Boulder, USA).

We then calculated the probability of sea ice occurrence among locations over the 1979-2010

period, *i.e.*, we estimated for each pixel of the landscape layer the number of years with sea

ice divided by the number of years of sea ice survey. We focused on two time periods

biologically relevant for caribou, which represent opportunities for genetic exchanges among

populations, *e.g.*, pre-calving migration and calving season [May-June] and rutting period

[October-November] (Boulet et al. 2007, Yannic et al. 2014). Finally, we assigned a

resistance value of 1 for landmass and sea ice (see Jenkins et al. 2016), and tested a varying

resistance value for sea water set between 2 and 1024, and weighted for the probability of

sea ice occurrence. To determine seawater resistance, we calculated pairwise distances

between populations following circuit theory on each resistance surface using the

commuteDistance function implemented in the '*gdistance*' 1.1-4 R package (R Development

Core Team 2016), and then correlated geographic distance with genetic distance with the

MMRR R function (Wang 2013). This approach identifies a peak of support for the

landscape resistance surface that better explains genetic differentiation (Graves et al. 2013,

Shirk et al. 2010), *i.e.*, the model with the highest correlation between resistance distance and

genetic differentiation (R^2; see Fig. A3). Because resistance distance models based on May-

June and October-November raster of sea-ice occurrence were highly correlated (all

Pearson's correlations $r > 0.92$), we only presented results based on the May-June period,

that is corresponding to the pre-calving migration and calving season. The location of the traditional calving ground of caribou herds is also generally see as a proxy for herd location, because of the philopatric behavior of caribou to calving sites (Boulet et al. 2007).
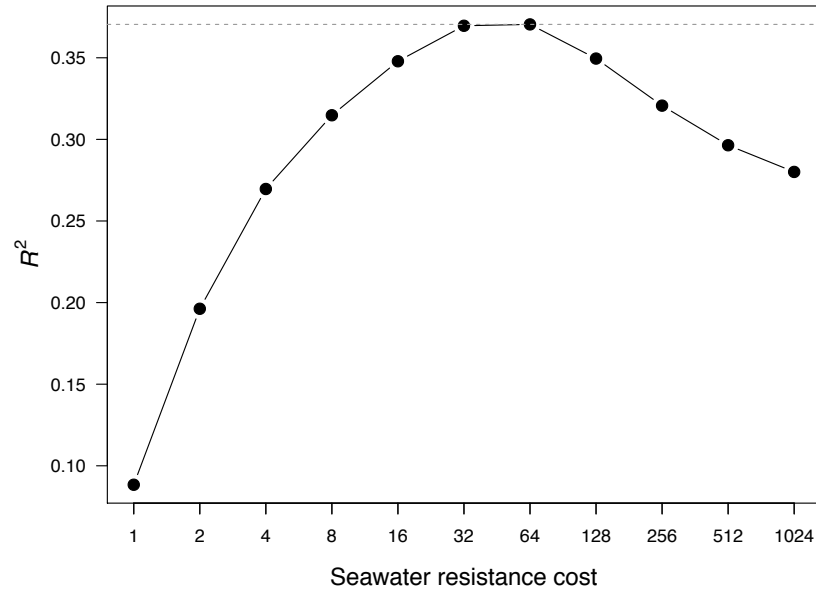
Figure A3. Plot of R^2 values obtained for MMRRs testing the effect of hypothetical raster surfaces on genetic differentiation (F_{ST}). Cost distances were obtained using circuit theory and an increasing resistance given to seawater [2:1024], weighted for the probability of sea ice occurrence. This approach identifies a peak of support for the model with the highest coefficient of determination (R^2) between geographic distance and genetic distance. The relationship peaks at a seawater resistance of 32. Note: all correlations were highly significant (all p-values <0.001). A resistance of 1 corresponds to a flat landscape.

8- Isolation-by-distance vs isolation-by-resistance

We used MMRR analyses to determine which alternative models among isolation-by-distance (IBD) and isolation-by-resistance (IBR) best fit the genetic data. We first ranked models according to their predictive power (higher R^2) in univariate models. Then we included competitive variables (*i.e.,* IBD based on Geodesic distance or a Flat landscape *versus* IBR; see Methods) in the multivariate MMRR model and compared estimator values and their significance.

We observed a higher simple correlation (higher R^2) for IBR in comparison to IBD univariate models (Table A3). When distance (IBD) and landscape-based resistance models (IBR) were included in multivariate MMRRs, we noticed a significant effect of landscape-based resistance distances on genetic differentiation (IBR), while IBD remained non-significant (Table A4). In conclusion, IBR systematically outperformed alternative IBD models.

Table A3 Univariate results of MMRR analyses for distance (IBD) (estimated on the basis of geodesic geographic distances and flat landscape considering equal resistance values for all pixels) and landscape-based resistance models (seawater resistance = 32) in caribou and reindeer.

			R^2	*p-value*	β±s.e	*t*	*p-value*
IBD	$F_{ST}\sim$	Geodesic	0.06	0.001	0.25±0.025	10.32	0.001
	$F_{ST}\sim$	Flat	0.09	0.001	0.42±0.034	12.43	0.001
IBR	$F_{ST}\sim$	Circuit	0.37	0.001	0.62±0.020	30.57	0.001

Table A4 Multivariate results of MMRR analyses for distance (IBD) (estimated on the basis of geodesic geographic distances and flat landscape considering equal resistance values for all pixels) and landscape-based resistance models (seawater resistance = 32) in caribou and reindeer. Corr.: *Pearson* correlation between independent variables.

IBR	**IBD**	R^2	*p-value*	β_{IBR}±s.e	*t*	*p-value*	β_{IBD}±s.e	*t*	*p-value*	*corr.*
$F_{ST}\sim$Circuit	+Geodesic	0.37	0.001	0.65±0.023	28.14	0.001	-0.08±0.023	-3.27	0.87	0.50
$F_{ST}\sim$Circuit	+Flat	0.37	0.001	0.62±0.023	26.66	0.001	0.00±0.032	0.025	0.49	0.49

9- Contribution of each environmental variable on PCA axes

Table A5 Contribution of each environmental variable on the first two PC axes obtained for PCAs performed considering different subsets of caribou and reindeer (*Rangifer tarandus*) populations. For each data set, the percentage of inertia of the first two axes is also provided. If all variables contributed equally, they would have a contribution of 1/22 or 4.54% (See Figure A1). A: at worldwide scale; B: excluding herds from Greenland and Svalbard; C: considering only migratory tundra, mountain, and boreal forest ecotypes; D: considering all North American herds; E: within the North-American lineage; F: within the Euro-Beringian lineage in North America; and G: within the Euro-Beringian lineage.

		A		B		C		D		E		F		G	
		PC-1	PC-2	PC-1	PC-2	PC-1	PC-2	PC-1	PC-2	PC-1	PC-2	PC-1	PC-2	PC-1	PC-2
	% variance	55.2	23.9	56.6	22.9	57.6	20.2	59.2	18.7	52.3	31.1	65.6	17.3	58.9	22.5
Elev.	alt	1.02	0.16	0.97	0.34	0.63	1.74	0.18	1.99	0.00	5.80	3.11	1.66	2.48	0.71
Veg.	NPP	2.74	9.40	2.57	10.13	3.50	9.34	5.05	4.97	4.27	3.18	4.60	5.84	0.95	13.49
	TREE	1.25	10.43	1.11	11.16	1.56	10.72	2.47	7.78	1.20	8.03	2.73	8.69	0.25	13.81
Temp.	BIO1	6.08	1.93	5.87	2.68	5.84	3.35	6.18	1.61	7.31	0.02	5.59	2.97	5.01	5.08
	BIO2	0.01	14.58	0.00	14.56	0.00	13.14	0.35	11.65	0.95	9.64	0.66	12.32	0.43	14.05
	BIO3	5.58	0.00	5.50	0.01	4.89	0.06	4.49	0.41	6.63	0.01	6.01	0.00	5.82	1.41
	BIO4	5.06	5.37	5.52	4.05	6.03	2.50	5.06	6.29	2.76	9.60	5.77	2.47	6.57	0.49
	BIO5	0.45	16.19	0.36	17.09	0.46	18.85	1.71	15.67	4.24	4.29	0.95	20.35	0.06	17.51
	BIO6	6.21	1.65	6.42	0.89	6.45	0.35	5.90	1.97	5.70	4.31	5.96	0.58	6.75	0.03
	BIO7	3.39	9.40	3.97	7.92	4.65	5.93	3.24	11.49	1.08	12.07	4.40	6.05	5.87	2.17
	BIO8	0.14	12.56	0.21	12.96	0.37	13.96	0.03	15.57	0.30	9.19	0.20	14.10	1.02	10.01
	BIO9	6.38	0.31	6.45	0.05	6.23	0.05	5.72	1.02	5.67	3.12	5.55	0.16	6.06	1.13
	BIO10	0.90	14.57	0.78	15.60	0.92	17.02	2.00	14.31	4.48	4.09	0.99	18.44	0.02	16.70
	BIO11	6.80	0.39	6.86	0.08	6.84	0.00	6.61	0.47	6.74	2.48	6.38	0.00	6.65	0.49
Precip.	BIO12	7.18	0.00	7.04	0.03	6.78	0.23	6.74	0.00	8.02	0.20	6.53	0.59	6.79	0.45
	BIO13	6.67	0.18	6.64	0.03	6.35	0.05	6.37	0.37	3.95	6.28	6.16	0.00	6.60	0.04
	BIO14	7.11	0.11	6.96	0.20	6.67	0.41	6.36	0.41	7.33	0.66	6.11	1.33	6.93	0.71
	BIO15	5.66	0.37	5.82	0.07	5.67	0.06	6.00	1.02	5.47	3.10	4.70	0.95	4.99	0.00
	BIO16	6.82	0.19	6.76	0.05	6.52	0.04	6.61	0.32	5.25	4.90	6.36	0.00	6.62	0.05
	BIO17	7.20	0.10	7.04	0.20	6.77	0.51	6.47	0.54	7.31	0.87	6.26	1.48	7.04	0.59
	BIO18	6.31	1.54	6.28	1.14	6.21	0.48	5.94	1.12	3.71	7.12	5.39	0.37	6.41	0.29
	BIO19	7.03	0.58	6.89	0.78	6.66	1.19	6.52	1.02	7.62	1.05	5.60	1.64	6.67	0.80

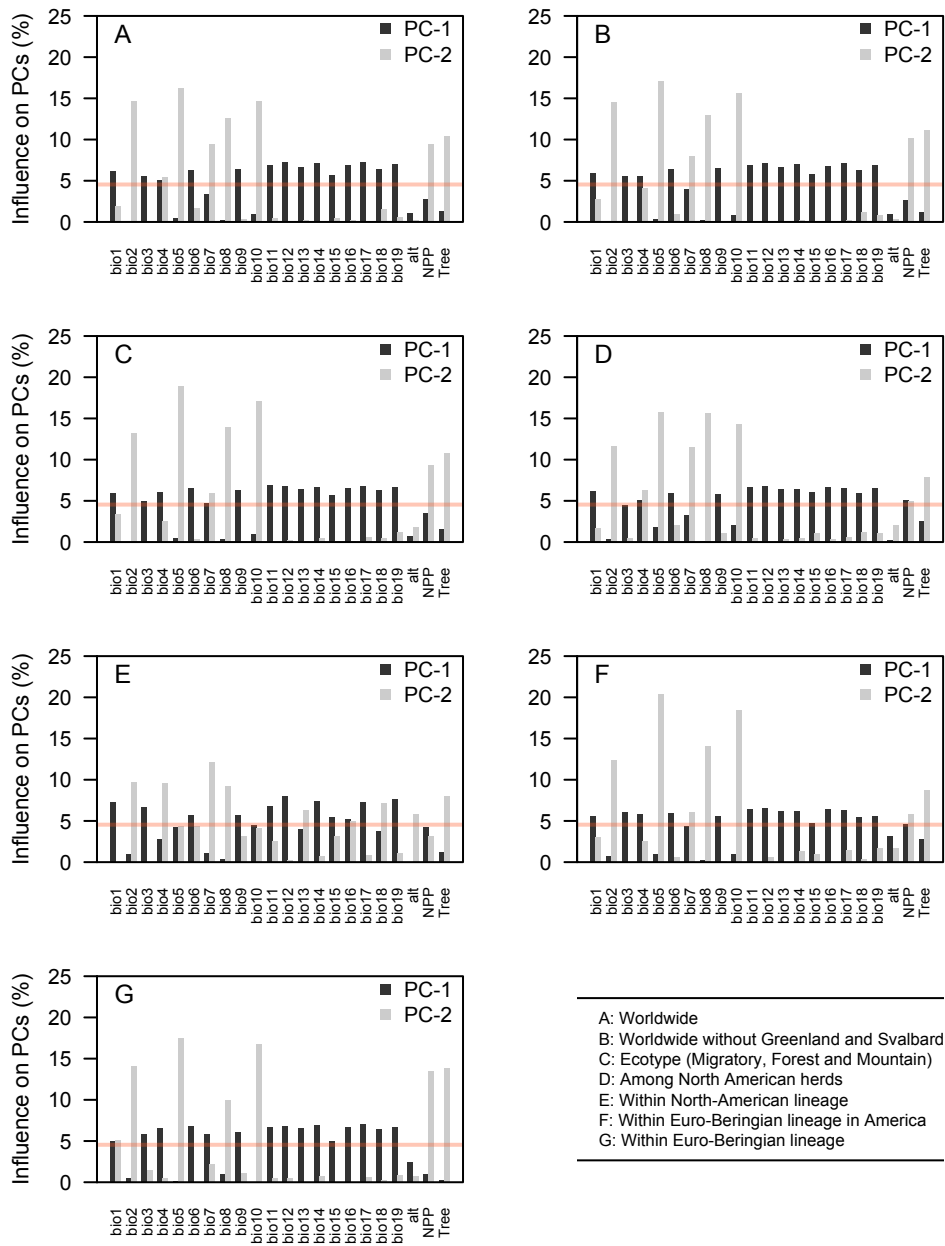## 10- Influence of environmental variables on PCA axes

Figure A4 Influence of environmental variables on the first two PC axes obtained for the different subsets of caribou and reindeer (*Rangifer tarandus*) populations. Axis 1 explained between 52.3% and 65.6% of variance and Axis 2 between 17.3% and 31.1%. If all the 22 variables had contributed equally, they would have had a contribution of 1/22 or 4.54% (red line).

11- Scatterplots of principal component analysis and environmental hierarchical clustering
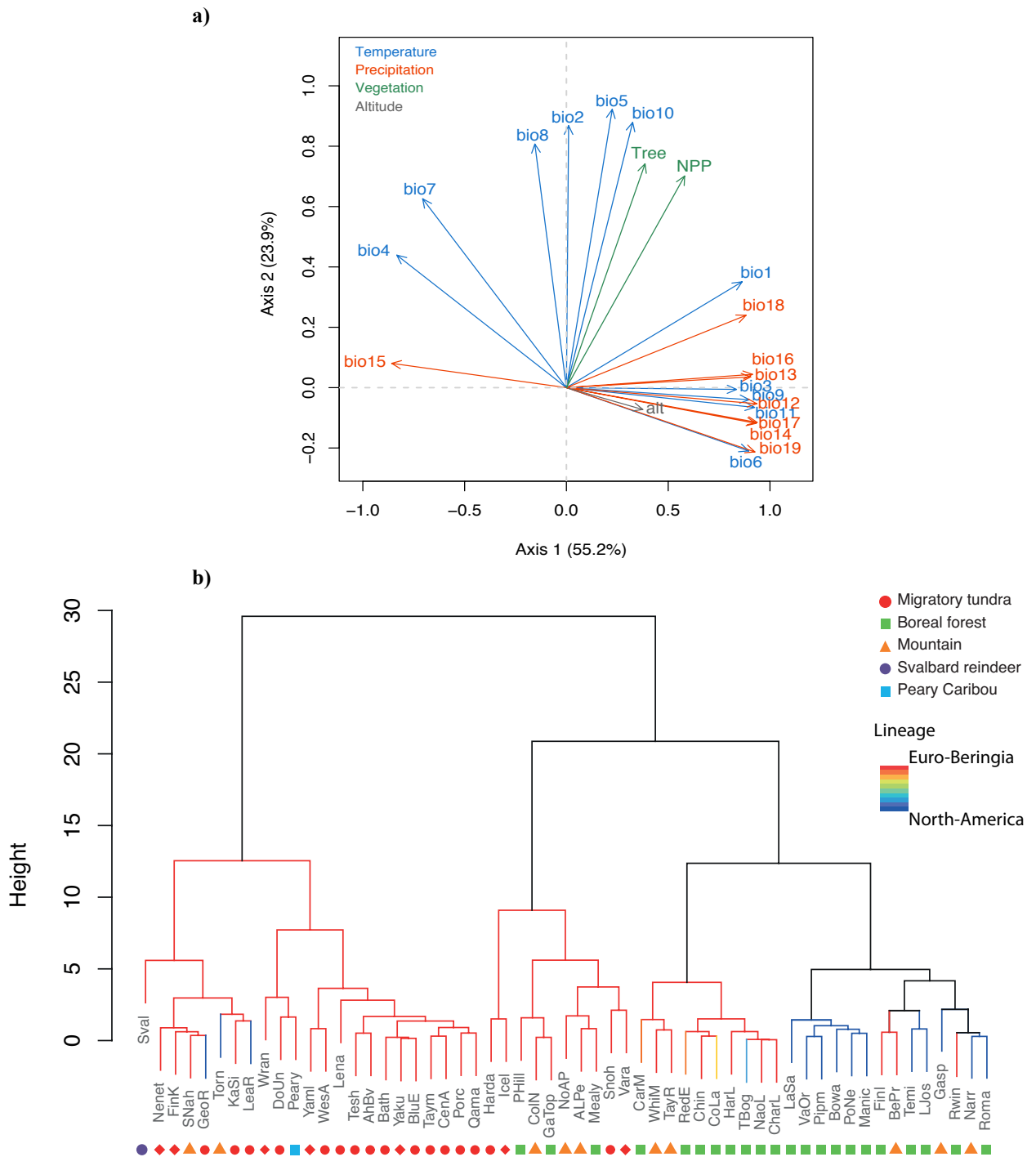
a)

b)

Figure A5 a) Scatterplots of a principal component analysis representing coefficients for each indicator variables used to estimate the environmental dissimilarity latent variables and **b)** Environmental hierarchical clustering of populations of caribou and reindeer (*Rangifer tarandus*) herds and ecotypes across the species' Holarctic distribution. Clustering was based on the PCA scores performed with the 22 environmental variables listed in Table A2. Clustering was obtained with the *Ward's* minimum variance method ("ward.D2") as implemented in the *hclust* function in R. The colors of the branches correspond to the Bayesian membership of each population to the North American (blue) and Euro-Beringian (red) lineages, respectively, obtained with STRUCTURE for *K*=2. Red diamonds correspond to introduced or semi-domestic migratory caribou-reindeer.

12- Model-averaged parameter estimates

Table A6 Model-averaged parameter estimates (β) with their unconditional standard errors (se) and 95% confidence intervals (95% CI) quantifying the effects of geography (isolation-by-resistance, *IBR*), different environmental variables (npp, tree, elevation, bioclimatic pc1 and pc2), harmonic mean of population size (*Nc*), and lineage membership (lineage) on genetic differentiation of caribou and reindeer (*Rangifer tarandus*) herds and ecotypes across the species' Holarctic distribution. Analyses are presented for the complete dataset (Worldwide), excluding the isolated populations from Greenland and Svalbard and focusing on certain populations according to their membership to different geographic regions, main genetic lineages or ecotype designations. Continuous variables were standardized to a mean of zero and a standard deviation of one. The number of herds in each dataset is also indicated. Adjusted *R*-squared were obtained from multiple linear regression models including all predictive factors. Estimates were considered as significant (bold type) when the one-sided 95% CI did not overlap zero and by randomization tests performed with MMRR.

	N	R^2	IBR β	se	95% CI	npp β_{npp}	se	95%CI	tree β_{tree}	se	95% CI	elev β_{elev}	se	95%CI	pc1 β_{pc1}	se	95% CI	pc2 β_{pc2}	se	95%CI	Nc β_{Nc}	se	95% CI	lineage $\beta_{lineage}$	se	95% CI
FST																										
A	53	0.46	**0.56**	**0.02**	**[0.52; +∞]**	0.12	0.03	[0.07; +∞]	-0.04	0.03	[-0.09; +∞]	-0.05	0.02	[-0.09; +∞]	-0.15	0.02	[-0.19; +∞]	**0.17**	**0.02**	**[0.13; +∞]**	0.00	0.02	[-∞; 0.04]	**0.28**	**0.04**	**[0.21; +∞]**
B	51	0.70	**0.59**	**0.02**	**[0.57; +∞]**	**0.19**	**0.02**	**[0.16; +∞]**	0.01	0.02	[-0.02; +∞]	-0.02	0.02	[-0.04; +∞]	-0.08	0.02	[-0.11; +∞]	**0.12**	**0.02**	**[0.09; +∞]**	-0.05	0.02	[-∞; -0.02]	**0.71**	**0.03**	**[0.66; +∞]**
C	43	0.65	**0.45**	**0.02**	**[0.41; +∞]**	**0.25**	**0.03**	**[0.20; +∞]**	0.04	0.02	[-0.00; +∞]	-0.01	0.02	[-0.05; +∞]	-0.20	0.02	[-0.24; +∞]	-0.04	0.02	[-0.08; +∞]	**-0.13**	**0.02**	**[-∞; -0.09]**	**0.95**	**0.04**	**[0.88; +∞]**
D	39	0.64	**0.49**	**0.03**	**[0.45; +∞]**	**0.25**	**0.03**	**[0.20; +∞]**	0.02	0.03	[-0.02; +∞]	-0.01	0.02	[-0.05; +∞]	-0.20	0.03	[-0.24; +∞]	0.02	0.02	[-0.02; +∞]	**-0.11**	**0.02**	**[-∞; -0.07]**	**0.88**	**0.05**	**[0.80; +∞]**
E	17	0.58	**0.93**	**0.08**	**[0.80; +∞]**	**0.25**	**0.06**	**[0.15; +∞]**	0.03	0.07	[-0.09; +∞]	0.04	0.06	[-0.05; +∞]	-0.30	0.08	[-0.43; +∞]	-0.16	0.06	[-0.26; +∞]	**-1.21**	**0.59**	**[-∞; -0.25]**			
F	22	0.45	0.28	0.06	[0.18; +∞]	0.07	0.08	[-0.06; +∞]	**0.25**	**0.06**	**[0.15; +∞]**	-0.04	0.06	[-0.13; +∞]	0.19	0.06	[0.09; +∞]	**0.20**	**0.05**	**[0.11; +∞]**	**-0.25**	**0.06**	**[-∞; -0.15]**			
G	34	0.68	**0.81**	**0.03**	**[0.76; +∞]**	0.12	0.03	[0.06; +∞]	0.04	0.04	[-0.02; +∞]	0.04	0.03	[0.00; +∞]	-0.10	0.03	[-0.15; +∞]	**0.22**	**0.03**	**[0.17; +∞]**	-0.05	0.03	[-∞; 0.00]			
A	53	0.62	**0.56**	**0.02**	**[0.53; +∞]**	0.03	0.02	[0.01; +∞]	0.00	0.02	[-0.04; +∞]	0.05	0.01	[0.03; +∞]	0.00	0.01	[-0.03; +∞]	**0.15**	**0.02**	**[0.13; +∞]**	0.00	0.02	[-∞; 0.02]	**0.42**	**0.03**	**[0.37; +∞]**
B	51	0.67	**0.52**	**0.02**	**[0.49; +∞]**	0.06	0.02	[0.03; +∞]	0.02	0.02	[-0.02; +∞]	**0.08**	**0.01**	**[0.06; +∞]**	0.03	0.01	[0.00; +∞]	**0.11**	**0.01**	**[0.09; +∞]**	-0.01	0.02	[-∞; 0.01]	**0.52**	**0.03**	**[0.47; +∞]**
C	43	0.71	**0.40**	**0.02**	**[0.37; +∞]**	**0.08**	**0.02**	**[0.04; +∞]**	0.04	0.02	[0.01; +∞]	**0.09**	**0.01**	**[0.07; +∞]**	0.01	0.02	[-0.02; +∞]	-0.01	0.02	[-0.03; +∞]	**-0.09**	**0.02**	**[-∞; -0.07]**	**0.72**	**0.03**	**[0.67; +∞]**
D	39	0.72	**0.47**	**0.03**	**[0.42; +∞]**	0.04	0.02	[0.00; +∞]	0.05	0.02	[0.01; +∞]	**0.11**	**0.02**	**[0.08; +∞]**	**0.07**	**0.02**	**[0.03; +∞]**	0.03	0.02	[0.00; +∞]	**-0.07**	**0.02**	**[-∞; -0.04]**	**0.55**	**0.04**	**[0.48; +∞]**
E	17	0.62	**1.03**	**0.08**	**[0.90; +∞]**	0.03	0.05	[-0.04; +∞]	0.06	0.05	[-0.02; +∞]	0.04	0.04	[-0.03; +∞]	-0.02	0.05	[-0.11; +∞]	-0.20	0.05	[-0.28; +∞]	**-1.34**	**0.42**	**[-∞; -0.66]**			
F	22	0.55	**0.31**	**0.05**	**[0.23; +∞]**	0.03	0.05	[-0.05; +∞]	0.10	0.03	[0.05; +∞]	0.06	0.03	[0.01; +∞]	0.06	0.04	[0.00; +∞]	**0.15**	**0.03**	**[0.10; +∞]**	**-0.24**	**0.03**	**[-∞; -0.18]**			
G	34	0.48	**0.52**	**0.03**	**[0.47; +∞]**	0.02	0.03	[-0.03; +∞]	0.05	0.03	[0.00; +∞]	0.08	0.03	[0.04; +∞]	-0.04	0.03	[-0.09; +∞]	**0.20**	**0.03**	**[0.16; +∞]**	-0.06	0.03	[-∞; -0.01]			

A: at worldwide scale; B: excluding herds from Greenland and Svalbard; C: considering only migratory tundra, mountain and boreal forest ecotypes; D: considering all North American herds; E: within the North American lineage; F: within the Euro-Beringian lineage in North America; and G: within the Euro-Beringian lineage

13- Relative contributions of predictive factors on genetic differentiation
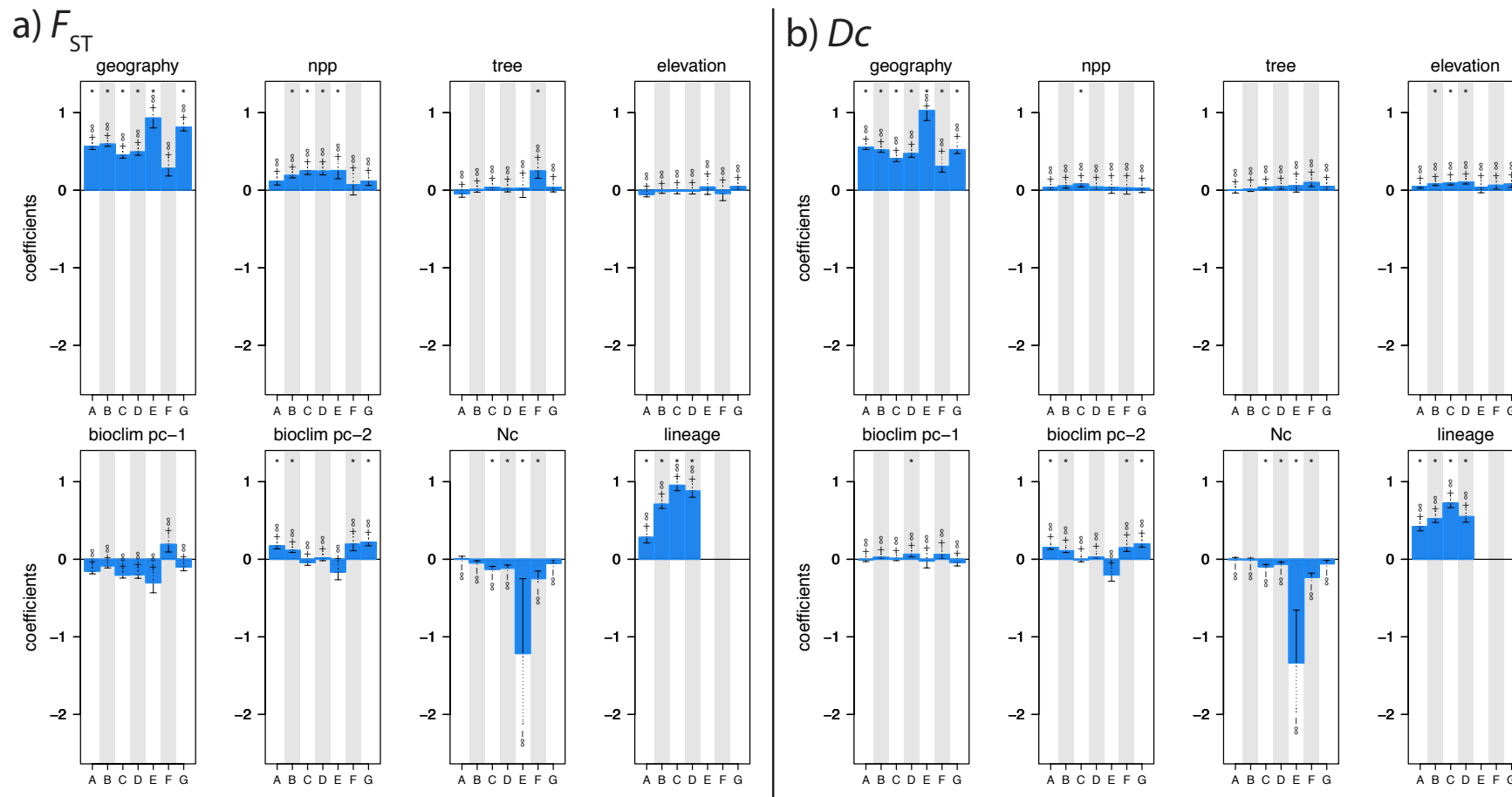

Figure A6 Relative contributions of geography (isolation-by-resistance, *IBR*), different environmental variables (npp, tree, elevation, bioclimatic pc1 and pc2), harmonic mean of population size (*Nc*), and lineage membership (lineage) as explanatory variables to genetic differentiation of caribou and reindeer (*Rangifer tarandus*) herds and ecotypes across the species' Holarctic distribution. The dependent variables are a) F_{ST} and b) *Dc* chord distance. A: at worldwide scale; B: excluding herds from Greenland and Svalbard; C: considering only migratory tundra, mountain and boreal forest ecotypes; D: considering all North American herds; E: within the North American lineage; F: within the Euro-Beringian lineage in North America; and G: within the Euro-Beringian lineage. Barplots depict effect sizes and 95% confidence intervals (95% CI) for each parameter. Estimates were considered as significant (asterisk) when the 95% CI did not overlap zero and by randomization tests performed with MMRR.

14- References

Balkenhol, N. et al. 2009. Statistical approaches in landscape genetics: an evaluation of methods for linking landscape and genetic data. - Ecography 32: 818-830.

Boulet, M. et al. 2007. Integrative use of spatial, genetic, and demographic analyses for investigating genetic connectivity between migratory, montane, and sedentary caribou herds. - Mol. Ecol. 16: 4223-4240.

Burnham, K. P. and Anderson, D. R. 2002. Model selection and multimodel inference: a practical information-theoretic approach. - Springer-Verlag.

CARMA 2016. CircumArctic Rangifer Monitoring and Assessment Network: status of herds. Available from http://www.carmanetwork.com/display/public/Herds.

Cavalli-Sforza, L. L. and Edwards, A. W. F. 1967. Phylogenetic analysis: models and estimation procedures. - Am. J. Hum. Genet. 19: 233-257.

Couturier, S. and Mitchell Foley, J. 2014. First scientific data on herd size and population dynamics of the Torngat Mountains caribou herd. Torngat Wildlife, Plants and Fisheries Secretariat.

DeFries, R. et al. 2000. Kilometer tree cover continuous fields 1.0, Department of Geography, University of Maryland, College Park, Maryland.

Environment Canada 2012. Recovery Strategy for the Woodland Caribou (*Rangifer tarandus caribou*), Boreal population, in Canada. - In: Species at Risk Act Recovery Strategy Series (ed), Environment Canada, p xi + 138 pp.

Équipe de rétablissement du caribou forestier du Québec 2013. Plan de rétablissement du caribou forestier (*Rangifer tarandus caribou*) au Québec - 2013-2023. Ministère du Développement durable, de l'Environnement, de la Faune et des Parcs du Québec, p 110 pp.

Geffen, E. et al. 2007. Sea ice occurrence predicts genetic isolation in the Arctic fox. - Mol. Ecol. 16: 4241-4255.

Golovatin, M. G. et al. 2012. Effect of reindeer overgrazing on vegetation and animals of tundra ecosystems of the Yamal peninsula. - Czech Polar Reports 2: 80-91.

Graves, T. A. et al. 2013. Current approaches using genetic distances produce poor estimates of landscape resistance to interindividual dispersal. - Mol. Ecol. 22: 3888-3903.

Guillot, G. and Rousset, F. 2013. Dismantling the Mantel tests. - Methods in Ecology and Evolution 4: 336–344.

Hanks, E. M. and Hooten, M. B. 2013. Circuit theory and model-based inference for landscape connectivity. - Journal of the American Statistical Association 108: 22-33.

Hedrick, P. W. 2005. A standardized genetic differentiation measure. - Evolution 59: 1633-1638.

Hegel, T. M. and Russell, K. 2013. Status of northern mountain caribou (*Rangifer tarandus caribou*) in Yukon, Canada. - Rangifer Special Issue 33: 59-70.

Henden, J.-A. et al. 2011. Population dynamics of tundra voles in relation to configuration of willow thickets in southern arctic tundra. - Polar Biol. 34: 533-540.

Hijmans, R. J. et al. 2005. Very high resolution interpolated climate surfaces for global land areas. - International Journal of Climatology 25: 1965–1978.

Jaquiéry, J. et al. 2011. Inferring landscape effects on dispersal from genetic distances: how far can we go? - Mol. Ecol. 20: 692-705.

Jenkins, D. A. et al. 2016. Loss of connectivity among Peary caribou following sea ice decline. - Biol. Lett. 12: 20160235.:

Johnsen, K. I. et al. 2015. Seeing like the state or like pastoralists? Conflicting narratives on the governance of Sami reindeer husbandry in Finnmark, Norway. - Norsk Geografisk Tidsskrift-Norwegian Journal of Geography 69: 230-241.

Jordhøy, P. et al. 2012. Villreinen i Snøhetta-og Knutshøområdet. Status og leveområde. NINA, p 120.

Jost, L. 2008. GST and its relatives do not measure differentiation. - Mol. Ecol. 17: 4015-4026.

Kucharik, C. J. et al. 2000. Testing the performance of a dynamic global ecosystem model: Water balance, carbon balance and vegetation structure. - Global Biogeochemical Cycles 14: 795-825.

Lalonde, M. and Michaud, J. 2013. Inventaire aérien de la population de caribou de la Gaspésie (*Rangifer tarandus caribou*), Automne 2012., p 19 pp.

Leblond, M. et al. 2016. Caribou, water, and ice – fine-scale movements of a migratory arctic ungulate in the context of climate change. - Movement Ecology 4: 1-12.

Legendre, P. and Fortin, M. 2010. Comparison of the Mantel test and alternative approaches for detecting complex multivariate relationships in the spatial analysis of genetic data. - Molecular Ecology Resources 10: 831-844.

MAF 2007. Management Plan for the Wild Forest Reindeer Population in Finland.

Mager, K. H. et al. 2014. Population structure over a broad spatial scale driven by non-anthropogenic factors in a wide-ranging migratory mammal, Alaskan caribou. - Mol. Ecol. 23: 6045-6057.

McCullagh, P. 2009. Marginal likelihood for distance matrices. - Statistica Sinica 19: 631-649.

McRae, B. H. 2006. Isolation by resistance. - Evolution 60: 1551-1561.

McRae, B. H. and Beier, P. 2007. Circuit theory predicts gene flow in plant and animal populations. - Proc Natl Acad Sci USA 104: 19885-19890.

Meirmans, P. G. and Hedrick., P. W. 2011. Measuring differentiation: Gst and related statistics. - Mol. Ecol. Resour. 11: 5-18.

Meirmans, P. G. and Van Tienderen, P. H. 2004. GENOTYPE and GENODIVE: two programs for the analysis of genetic diversity of asexual organisms. - Mol. Ecol. Notes 4: 792-794.

Miller, F. L. 1995. Inter-island water crossings by Peary caribou, south-central Queen-Elizabeth islands. - Arctic 48: 8-12.

Miller, F. L. et al. 2005. Sea-ice crossings by caribou in the south-central Canadian Arctic Archipelago and their ecological importance. - Rangifer 25: 77-88.

Morrison, S. F. et al. 2012. Projection of woodland caribou populations in Newfoundland: An application of Leslie – Matrix population models to predict future of Newfoundland caribou herds (2010 – 2035). - In: 003, T. B. N. (ed), Sustainable Development and Strategic Science, Department of Environment and Conservation, Government of Newfoundlandand Labrador. St. John's, NL, Canada.

Poole, K. G. et al. 2010. Sea ice and migration of the Dolphin and Union Caribou herd in the Canadian Arctic: An Uncertain Future. - Arctic 63: 418-428.

R Development Core Team 2016. R version 3.2.3: A language and environment for statistical computing. R Foundation for Statistical Computing.

Reimers, E. et al. 2011. Vigilance and fright behaviour in the insular Svalbard reindeer (Rangifer tarandus platyrhynchus). - Canadian Journal of Zoology-Revue Canadienne De Zoologie 89: 753-764.

Russell, D. E. and Gunn, A. 2013. "Migratory Tundra Rangifer" - 20 November 2013. NOAA Arctic Research Program.

Schmelzer, I. 2011. An estimate of population size and trend for the Lac Joseph caribou herd and the greater region of south-central Labrador: Results of a large-scale aerial census conducted during March 2009. Wildlife Division Report, Department of Environment and Conservation, Corner Brook, NL, p 24.

Schwartz, M. K. et al. 2009. Wolverine gene flow across a narrow climatic niche. - Ecology 90: 3222-3232.

Serrouya, R. et al. 2012. Population size and major valleys explain microsatellite variation better than taxonomic units for caribou in western Canada. - Mol. Ecol. 21: 2588-2601.

Sheremetev, I. S. et al. 2014. Extinction of large herbivore mammals: niche characteristics of the musk ox *Ovibos moschatus* and the reindeer *Rangifer tarandus* coexisting in isolation. - Biology Bulletin Reviews 4: 433-442.

Shirk, A. J. et al. 2010. Inferring landscape effects on gene flow: a new model selection framework. - Mol. Ecol. 19: 3603-3619.

Wang, I. J. 2013. Examining the full effects of landscape heterogeneity on spatial genetic variation: a multiple matrix regression approach for quantifying geographic and ecological isolation. - Evolution 67: 3403-3411.

Weckworth, B. V. et al. 2013. Preferred habitat and effective population size drive landscape genetic patterns in an endangered species. - Proc R Soc Lond, Ser B: Biol Sci 280: 20131756.

Weir, B. S. and Cockerham, C. C. 1984. Estimating *F*-statistics for the analysis of population structure. - Evolution 38: 1358-1370.

Yannic, G. et al. 2014. Temporally dynamic habitat suitability predicts genetic relatedness among caribou. - Proc R Soc Lond, Ser B: Biol Sci 291: 20140502.