Supporting Information

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SI Text

Archaeological Sites and Samples. *Trou Al'Wesse (Belgium).* A total of 60 collared lemming mandibles were obtained from the current excavations on the terrace of Trou Al'Wesse (TAW; 50.421, 5.294). Located 50 m from the Hoyoux River in the Belgian Ardennes, this is a stratified prehistoric cave site with a long stratigraphic sequence containing Mousterian, Aurignacian, Mesolithic, and Neolithic occupations with intervening periods rich in faunal material (1, 2).

Samples were sourced from meter squares (e.g., M4) dug stratigraphically, each stratum dug in a series of 3- to 5-cm-thick spits. Each square is divided into 50-cm subsquares to control the context of sieved material; the coordinates of artifacts and bones larger than 1 cm are recorded using a Total Station. To examine faunal response to events surrounding the Last Glacial Maximum (LGM), and to remain within accepted limits for radiocarbon dating, collared lemming samples were obtained from pre-LGM strata (16 and 14) as well as post-LGM stratum 12, up to and including transition into the warmer climate of the Holocene (stratum 4b) (3).

Marie-Jeanne (Belgium). A total of 23 collared lemming mandibles were obtained from Caverne Marie-Jeanne (CMJ; 50.130, 4.476), an archeological cave site in the Belgian Ardennes, located 25 m above the right bank of the Féron, a small tributary of the Meuse River near Hastiere-Lavaux. M. Glibert of the Royal Belgian Institute of Natural Sciences initiated excavations of the cave in 1943 and found the deposits to be largely composed of clay, silt, and sand that had been washed into the cave along joints. Paleontological and archaeological objects recovered from the site suggest a Weichselian date, largely pre-Aurignacian in age. Artifacts attributable to the Mousterian were also discovered at the site, but too few to suggest a significant prehistoric human occupation (4). Collared lemming remains however, were found in all horizons, with samples used in this study originating from particularly abundant horizons: 2, 4, 5a, 5b, and 6 (5).

Bridged Pot (United Kingdom). A total of five collared lemming mandibles were obtained from Bridged Pot Cave (BPC; 51.234, –2.680), an archeological site located in Ebbor Gorge, Somerset, England. Excavation of the site was carried out by H. E. Balch, 1926–1929, and continued in 1958 by C. B. M. McBurney (6). Samples were sourced from an established stratigraphic layer (B), rich in small mammal remains and associated with the Younger Dryas ca. 12.8–11.5 Kyr BP (7).

Materials from each of the three locations were sieved on site, sealed in bags, and maintained at a constant temperature to limit contamination and DNA degradation. In the laboratory, mandibular samples were identified to species level through morphological characters of the M_1, species specific to the collared lemming (8).

DNA Extraction and Sequencing. A total of 88 collared lemming mandibles were sourced for these analyses. DNA extractions were conducted in two dedicated ancient DNA laboratories: Royal Holloway, University of London (TAW and BPC samples) and the Swedish Museum of Natural History, Stockholm (CMJ samples). Samples were drilled or ground into a fine powder, with ~10–50 mg used in the DNA extraction process. DNA extraction protocol followed Yang et al. (9) using proteinase K to digest bone powders (modified with the inclusion of 1M urea in the extraction buffer) and silica spin columns to purify DNA. Mitochondrial DNA (mtDNA) was amplified using overlapping fragments spanning 780 base pairs of the cytochrome *b* (cyt *b*) region. Nine primer pairs were designed specifically for this study, each pair amplifying short (130–180 bp) overlapping fragments (Table S1). An additional forward primer (D2) was used for two samples (44a and 50a) following poor amplification results from an initial primer pair (D). PCR reactions (TAW and BPC samples) were performed using a final concentration of 1 × PCR buffer, 0.2 μM of each primer, 250 μM dNTPs, 2 mM $MgSO_4$, 1 mg/mL BSA, 1 Unit Platinum Taq DNA polymerase high fidelity, purified water, and 2 μL of DNA extract in a 25 μL mix. PCR conditions were 5 min at 95 °C, followed by 55 cycles of 1 min at 92 °C, 1 min at 49 °C, 50 °C or 51 °C (dependent on primer pair specifications), 1 min at 68 °C, and with a final extension of 5 min at 68 °C. PCR reactions (CMJ samples) were performed using a final concentration of 1 × PCR buffer, 0.2 μM of each primer, 200 μM dNTPs, 2.5 mM $MgCl_2$, 0.1 mg/mL BSA, 0.4 Units HotStar Taq DNA polymerase (Qiagen), purified water, and 2 μL of DNA extract in a 25 μL mix. PCR conditions were 10 min at 95 °C, followed by 55 cycles of 30 s at 94 °C, 30 s at 49 °C, 50 °C or 51 °C (dependent on primer pair specifications), 30 s at 72 °C, and with a final extension of 7 min at 72 °C.

Amplicons were purified using Exonuclease I and Shrimp Alkaline Phosphatase (TAW and BPC samples) and Exonuclease I and FastAP Thermosensitive Alkaline Phosphatase (CMJ samples). Sequencing reactions (TAW and BPC samples) were performed by Macrogen using a high-throughput genetic analysis sequencer (ABI3730XL) and at the Molecular Systematics laboratory at the Swedish Museum of Natural History (Stockholm, Sweden) using an ABI3130XL automated sequencer (CMJ samples). Sequencing chromatograms were assembled and analyzed using Sequencher 4.0 analysis software (Gene Codes Corporation) and Geneious 5.5.4 (10). Throughout our procedures, protocols to prevent contamination and ensure accurately coded (undamaged) mtDNA were followed: isolation of work areas, negative controls, reduced fragment length amplification, and repeated PCR amplification and sequencing of fragments.

1. Miller R, Stewart J, Zwyns JN, Otte M (2009) in *Chronology and Evolution within the Mesolithic of North-West Europe: Proceedings of an International Meeting, Brussels, May 30th–June 1st 2007*, eds Crombé P, Van Strydonck M, Sergant J, Boudin M, Bats M (Cambridge Scholars Publishing, Newcastle upon Tyne, UK), pp. 287–306.
2. Miller R, Zwyns N, Otte M, Stevens C, Stewart J (2012) La séquence mésolithique et néolithique du Trou Al'Wesse (Belgique): Résultats pluridisciplinaires. *Anthropologie* 116:99–126.
3. Pirson S (1999) Étude sédimentologique préliminaire au Trou Al'Wesse (Modave, Belgique). Bulletin de la Société royale belge d'études géologiques et archéologiques, (Les Chercheurs de la Wallonie) 39:115–162.
4. Ballmann P, et al. (1980) in *La Caverne Marie-Jeanne (Hastiere-Lavaux, Belgique)*, eds Gautier A, de Heinzelin J (Institut Royal des Sciences Naturelles de Belgique, Belgium) Memoire 177:3–24.
5. Ballmann P, et al. (1980) in La Caverne Marie-Jeanne (Hastiere-Lavaux, Belgique), eds Gautier A, de Heinzelin J (Institut Royal des Sciences Naturelles de Belgique, Belgium) Memoire 177:3–24.
6. Price CR (2003) Late Pleistocene and Early Holocene small mammals in South West Britain: Environmental and taphonomic implications and their role in archaeological research. (Archaeopress, Oxford, UK) British Archaeological Reports British Series 347.
7. Price CR (2003) Late Pleistocene and Early Holocene small mammals in South West Britain: Environmental and taphonomic implications and their role in archaeological research. British Archaeological Reports 347.
8. Nadachowski A (1982) *Late Quaternary Rodents of Poland with Special Reference to Morphotype Dentition Analysis of Voles* (Polska Akademia Nauk, Kraków).
9. Yang DY, Eng B, Waye JS, Dudar JC, Saunders SR (1998) Technical note: Improved DNA extraction from ancient bones using silica-based spin columns. *Am J Phys Anthropol* 105(4):539–543.
10. Drummond AJ, et al. (2011) *Geneious v5.4* (Biomatters). Accessed January 10, 2012.

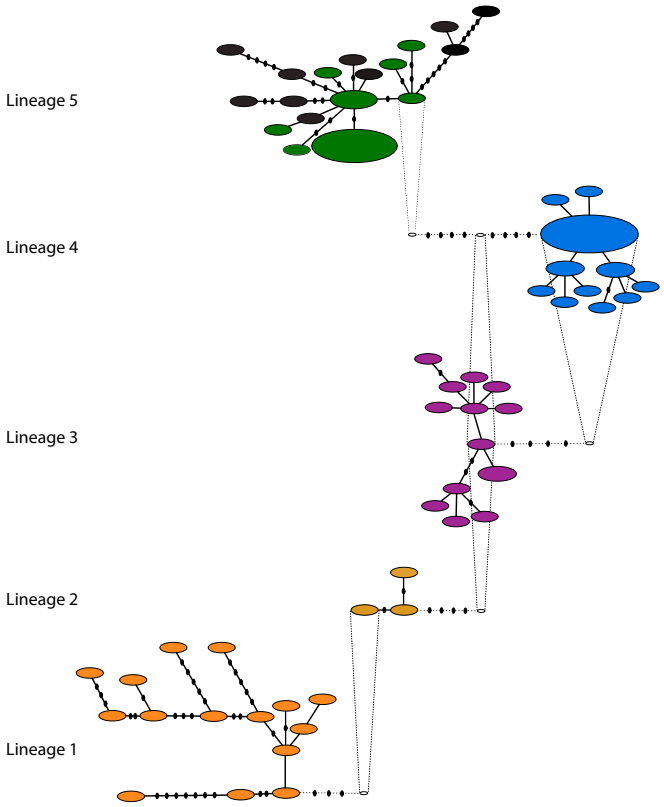

Fig. S1. Three-dimensional statistical parsimony network for *Dicrostonyx* mtDNA haplotypes (cyt *b*). Layers represent the different lineages identified by Bayesian phylogenetic analysis. Each circle represents one haplotype. Haplotype color corresponds to the most representative color from each lineage (Fig. 2), with modern haplotype circles M1–M10 colored black. Small black dots represent missing haplotypes. Small clear dots represent haplotypes that are missing from one particular layer but are present in the layer above or below. The size of each circle is proportional to haplotype frequency.

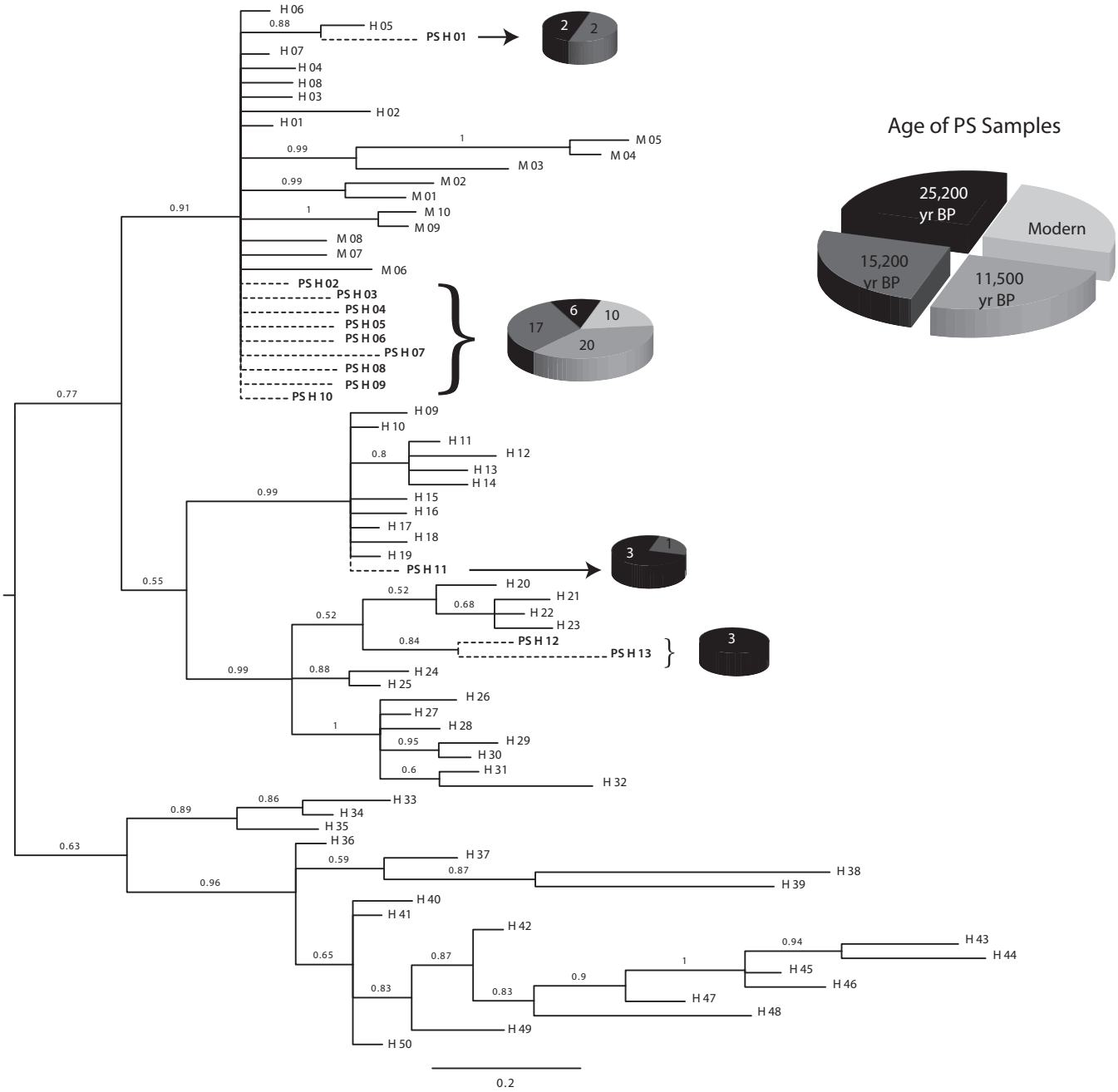

Fig. S2. Phylogeny for mtDNA haplotypes (cyt *b*) of *Dicrostonyx* combining our results and data from Pymva-Shor (1). Numbers above branches represent Bayesian posterior probabilities. The outgroup *Dicrostonyx hudsonius* is removed for display purposes. M, modern samples (GenBank); H, haplotype (ancient sample: present study); PS H and dashed branch line, haplotype from the Pymva-Shor study. Pie charts indicate details of the PS samples corresponding to each haplotype: segment color, sample ages in years Before Present; the number inside each segment represents number of samples per age group. Curly bracket indicates haplotypes that are combined into a single pie chart.

1. Prost S, et al. (2010) Influence of climate warming on arctic mammals? New insights from ancient DNA studies of the collared lemming *Dicrostonyx torquatus*. *PLoS ONE* 5(5):e10447.

Table S1. Details of the primer pairs used to amplify mtDNA (cytochrome *b*) from samples of *Dicrostonyx*

Primer name	Forward Sequence 5′ to 3′	Reverse Sequence 5′ to 3′	Annealing temp (°C)	Product		
				Start position	End position	Length (bp)
A	CATCTGATACAGCAACAGCATTCTC	GTAGATGCCTCGTCCTACGTGTAA	51	167	286	143
B	TAATAGCAACAGCATTCATAGG	CCCCCTCAGATTCATTCTAC	50	368	481	133
C	GGGGGCTTCTCAGTTGACAA	GGATTTTGTCTGCGTCGGAG	51	496	636	160
D	CTCGGAGACCCAGATAATT	GGAAGGTTATGAGGGCTAG	50	748	901	172
D2	ATATTCTCGGAGACCCAGA	GGAAGGTTATGAGGGCTAG	49	743	901	177
E	GCTCCCTACTTGGCCTATG	AGAATATGGAGGCTCCGTTT	50	101	252	171
F	GGAGCCTCCATATTCTTCATC	AAGGATATTTGTCCTCATGGG	50	256	399	164
G	CTATCAGCAATCCCCTACATC	GTTAGAGCCTGTTTCGTGAAG	51	448	598	171
H	GGCTCTAACAACCCATCAGGC	TAAGTGGGTTTGCAGGGGTGT	51	610	767	178
I	TAAACTCCGACGCAGAC	TGTGGTGGAGTATTAAGTGG	50	632	781	169

Product start and end positions represent the base pair position of the 3′ end of the forward and reverse primers respectively, within the mtDNA cytochrome *b* gene.

Table S2. Details of the samples of *Dicrostonyx* that successfully yielded the targeted 780 base pair region of mtDNA (cytochrome *b*) and modern *Dicrostonyx* sequence data obtained from GenBank

UI	Accession no.	Country	Site name	Stratigraphic position		
				Layer/horizon	Square/level	Spit
01_a	JX867564	United Kingdom	BPC			
02_a	JX867565	United Kingdom	BPC			
03_a	JX867566	United Kingdom	BPC			
03_b		United Kingdom	BPC			
03_c		United Kingdom	BPC			
04_a	JX867567	Belgium	TAW	12	M4D	6
05_a	JX867568	Belgium	TAW	12	M3	1
06_a	JX867569	Belgium	TAW	12	M3	1
06_b		Belgium	TAW	12	M3	1
06_c		Belgium	TAW	12	M3	1
06_d		Belgium	TAW	12	M3	1
06_e		Belgium	TAW	12	M3	1
06_f		Belgium	TAW	12	M3	2
06_g		Belgium	TAW	12	M3	2
06_h		Belgium	TAW	12	M4	5
06_i		Belgium	TAW	12	M4	5
06_j		Belgium	CMJ	2		
07_a	JX867570	Belgium	TAW	12	M3	1
08_a	JX867571	Belgium	TAW	12	M3	2
09_a	JX867572	Belgium	TAW	12	M4	5
09_b		Belgium	TAW	12	M4D	6
10_a	JX867573	Belgium	TAW	12	M4	5
10_b		Belgium	TAW	12	M4	5
10_c		Belgium	TAW	12	M4	5
10_d		Belgium	TAW	12	M4	5
10_e		Belgium	TAW	12	M4	5
10_f		Belgium	TAW	12	M4D	6
10_g		Belgium	TAW	12	M4D	6
10_h		Belgium	TAW	12	M4D	6
10_i		Belgium	TAW	12	M4D	6
10_j		Belgium	TAW	12	M4D	6
10_k		Belgium	TAW	12	M3	9
10_l		Belgium	TAW	4	K4	5B
10_m		Belgium	TAW	4	K4	5A
11_a	JX867574	Belgium	TAW	12	M4	5
11_b		Belgium	TAW	12	M4D	6
12_a	JX867575	Belgium	TAW	12	M4	5
13_a	JX867576	Belgium	TAW	12	M4D	6
14_a	JX867577	Belgium	TAW	12	M4D	6

Table S2. Cont.

UI	Accession no.	Country	Site name	Stratigraphic position		
				Layer/horizon	Square/level	Spit
15_a	JX867578	Belgium	TAW	12	M4	5
16_a	JX867579	Belgium	TAW	12	M4	5
17_a	JX867580	Belgium	TAW	12	M4D	6
18_a	JX867581	Belgium	TAW	12	M4D	6
19_a	JX867582	Belgium	TAW	12	M3	9
20_a	JX867583	Belgium	CMJ	2		
21_a	JX867584	Belgium	TAW	12	M3	9
22_a	JX867585	Belgium	TAW	12	M3	9
23_a	JX867586	Belgium	TAW	12	M4	6
24_a	JX867587	Belgium	TAW	12	M4	6
24_b		Belgium	TAW	12	M3	9
25_a	JX867588	Belgium	TAW	14	D7	16
26_a	JX867589	Belgium	TAW	14	D7	16
27_a	JX867590	Belgium	TAW	14	K6	9
28_a	JX867591	Belgium	TAW	14	K6	9
29_a	JX867592	Belgium	TAW	16	M7	16
30_a	JX867593	Belgium	TAW	14	K7	9
31_a	JX867594	Belgium	TAW	16	M7	16
32_a	JX867595	Belgium	TAW	12	M4	6
33_a	JX867596	Belgium	CMJ	3		
34_a	JX867597	Belgium	CMJ	5	A&B	
35_a	JX867598	Belgium	CMJ	5	A	
36_a	JX867599	Belgium	CMJ	5	A	
37_a	JX867600	Belgium	CMJ	3		
38_a	JX867601	Belgium	TAW	16	C7	19
39_a	JX867602	Belgium	CMJ	4		
40_a	JX867603	Belgium	CMJ	5	B	
41_a	JX867604	Belgium	CMJ	4		
42_a	JX867605	Belgium	CMJ	5	B	
43_a	JX867606	Belgium	CMJ	5	B	
44_a	JX867607	Belgium	CMJ	5	A	
45_a	JX867608	Belgium	CMJ	5	A	
46_a	JX867609	Belgium	CMJ	6		
47_a	JX867610	Belgium	CMJ	6		
48_a	JX867611	Belgium	CMJ	6		
49_a	JX867612	Belgium	CMJ	6		
50_a	JX867613	Belgium	CMJ	4		
M01	AJ238423	Russia				
M02	AJ131441	Russia				
M03	AJ238425	Russia				
M04	AJ238424	Russia				
M05	AJ131442	Russia				
M06	AF119275	Russia				
M07	AJ238421	Russia				
M08	AJ131439	Russia				
M09	AJ131440	Russia				
M10	AJ238422	Russia				
O	AJ238437	Canada				

UI M, modern; UI O, modern (used as an outgroup).

Table S3. Radiocarbon dates from samples of *Dicrostonyx* used in our analyses

UI	Site	AMS 14C Date (yr BP)	±	Calibrated age range BP (95.4%)	Median yr BP	Reference no,	Lineage
06_j	CMJ	12,275	55	14,850–13,925	14,165	OxA-24122	5
06_g	TAW	14,415	70	17,865–17,185	17,539	OxA-2354-15	5
07_a	TAW	15,150	120	18,641–18,021	18,287	OxA-2352-39	5
06_f	TAW	16,440	100	19,903–19,403	19,562	OxA-23565	5
08_a	TAW	16,980	110	20,443–19,609	20,166	OxA-2352-41	5
06_h	TAW	17,030	90	20,467–19,876	20,227	OxA-2354-14	5
11_a	TAW	17,520	120	21,329–20,422	20,859	OxA-23564	4
10_a	TAW	17,780	130	21,535–20,548	21,230	OxA-2352-40	4
10_c	TAW	17,780	120	21,533–20,553	21,238	OxA-23563	4
19_a	TAW	18,260	120	22,217–21,452	21,815	OxA-23567	4
20_a	CMJ	20,930	140	25,456–24,497	24,945	OxA-24123	3
24_a	TAW	22,500	190	27,894–26,327	27,237	OxA-2354-16	3
26_a	TAW	25,650	450	31,101–29,584	30,449	OxA-2352-11	3
23_a	TAW	26,300	380	31,351–30,356	30,917	OxA-2352-42	3
32_a	TAW	26,830	360	31,805–30,735	31,249	OxA-23566	3
35_a	CMJ	40,500	1,400	**47,501–42,364**	**44,513**	OxA-24119	2
34_a	CMJ	> 43,700				OxA-24121	2
39_a	CMJ	47,600	3,300	**63,308–42,622**	**49,601**	OxA-24115	1
41_a	CMJ	43,000	1,900	**49,972–44,453**	**46,752**	OxA-24117	1
40_a	CMJ	43,600	2,100	**NA–44,756**	**47,165**	OxA-24118	1
42_a	CMJ	44,400	2,300	**NA–45,131**	**47,571**	OxA-24120	1
46_a	CMJ	> 43,000				OxA-24124	1
50_a	CMJ	> 43,900				OxA-24116	1
45_s	TAW	Failed no yield					
28_a	TAW	Failed no yield					
25_a	TAW	Failed low yield					
38_a	TAW	Failed no yield					
31_a	TAW	Failed low yield					

Dates were calibrated using Oxcal v4.1 with the IntCal09 calibration curve. Dates in bold may extend the calibration range. NA, not available because of likely extension beyond the calibration range.

Table S4. Haplotype frequency (per age range years BP) of Pymva-Shor samples

PS H number	Accession no.	Haplotype frequency			
		Modern	11,500 (yr BP)	15,200 (yr BP)	25,200 (yr BP)
01	HM009006			2	2
02	HM008998	7	14	1	3
03	HM008999	3			
04	HM009000		2	7	1
05	HM009001		1		
06	HM009002		1		
07	HM009003		1		
08	HM009004		1		
09	HM009005		1		
10	HM009008			8	2
11	HM009007			1	3
12	HM009009				2
13	HM009010				1

Table S5. Bayesian derived timing of lineage presence (1–5) and turnover events (A–D) between lineages of *Dicrostonyx* from North-West Europe based on AMS dated samples

Lineage	Turnover event	Upper boundary (95.4%)	Lower boundary (95.4%)	Range for turnover events
1		50,766–46,002	49,168–44,733	
	A	49,168–44,733	47,624–42,990	48,386–43,817
2		47,624–42,990	45,613–33,777	
	B	45,613–33,777	37,577–30,931	42,938–31,631
3		37,577–30,931	25,243–22,043	
	C	25,243–22,043	22,894–21,300	24,479–21,564
4		22,894–21,300	21,344–20,423	
	D	21,344–20,423	21,062–20,114	21,200–20,269
5		21,062–20,114	14,907–11,396	

Dates are calibrated calendar ages (years BP) generated using Oxcal v4.1 with the IntCal09 calibration curve.