SUPPLEMENTARY TABLES

Supplementary Table S1: Summary of previous claims for Mesolithic domestic animals in northern Europe

Country	Site (dating)	Claim	Basis for questioning evidence	Earliest proven appearance of domesticates
Denmark	Dyrholm I (Classic Ertebølle)	Domestic cattle, based on lower M3s[57,58]	Re-evaluation[59] based on an increasing number of aurochs reference skeletons (overlap between small female aurochs and domestic cattle (sexual dimorphism))	16 domestic cattle from Åkonge (3900 *cal* BC)[61]
	Lollikhuse (Late Mesolithic / 5th millennium BC)	Domestic cattle, based on a single bone[60]	Identification of remains uncertain[6]	
Northern Germany	Rosenhof (late Ertebølle)	Domestic cattle, based on a mandibular M3, scapula (fused) and a distal metacarpal (fused)[62]	M3; sexual dimorphism[63,64] Scapula; dimension is subject to very considerable growth and an early fusion in life (thus juvenile aurochs) Metacarpal; isotope ratio in the range of contemporaneous aurochs[65], aDNA matches with native aurochs[22]	Domestic cattle at Wangels ~4100 *cal* BC[3,68]
		Domestic pig, based on a scapula (fusion unknown)[62]	Dimension is subject to very considerable growth[18]	
	Bregendtwendt-Förstermoor (Late Ertebølle)	Domestic cattle, based on a scapula (fusion unknown)[66]	Dimension is subject to very considerable growth[18]	
	Lietzow-Buddelin (Late Ertebølle)	Two caprine elements[67]	Elements may be intrusive from overlying layers[67]	
Poland	Dęby (6th millennium BC)	Domestic goats[69]	No longer accepted, new dating of the stratigraphy[70]	Domestic cattle at Dąbki ~4200 *cal* BC[71]

	Dąbki (Late Mesolithic)	Domestic cattle and pig[69]	No metrical evidence offered, re-evaluation suggests domestic cattle appear ~4200 *cal* BC[71]	
Netherlands	Hardinxveld-Giessendam De Bruin (Mesolithic 4700 *cal* BC)	Layer 2: three domestic animals Layer 3: 28 domestic animals (15 cattle, 3 pigs, 10 caprines)[72]	Cattle: none is directly dated, no metrical data no fusion points (carpals), post fusion growth (scapula, pelvis) or highly variable (phalanges) pig: none is directly dated, no metrical data caprine: none is directly dated, no metrical data[5]	Domestic animals from Swifterbant S3 (4100 *cal* BC)[75]
	Brandwijk-Kerkhof (Mesolithic 4700 *cal* BC)	Eight domestic cattle bones from layer A[73]	Layer A dated to 4900-4100 *cal* BC, was identified afterwards on the basis of ceramic temper, animal bones are not at the bottom of the layer[73]. No details on the bones, most are burnt, calcined, heavily weathered or poorly preserved[73].	
		79 domestic pigs from layer A[73]	The majority of the bones are heavily burnt[73]; no useful measurements presented[5]	
	Schockland P14 (layer 30 (4500 *cal* BC); layer 40/50 (4000 *cal* BC))	From layer 50, two pig upper M3s are claimed as domestic[74]	None is directly dated[5,74]	
		Two caprine fragments (second phalanx, scapula) from layer 30[74]	None is directly dated[5,74]	
Ireland	Ferriter`s Cove (~4300 *cal* BC)	Domestic cattle, two specimens[76,77]	None	Domestic cattle at Ferriter`s Cove (~4300 *cal* BC) and Kilgreany Cave (~4300 *cal* BC)[76,77]
	Kilgreany Cave (~4300 *cal* BC)	Domestic cattle, one specimen[76,77]	None	

Supplementary Table S2. Primers used to amplify the diagnostic 80-bp fragment of *Sus* mtDNA

Set	Primer name	Sequence	Fragment size
ANC1	ANC-F1*	CTTTAAAACAAAAAAACCCATAAAAA	128 bp
	ANC-R1*	TTAATGCACGACGTACATAGG	
PIG1	PIG1FOR*	CATTCCATTCGTATGCAAACC	173 bp
	ANC-R1*	TTAATGCACGACGTACATAGG	

All primers are listed in the 5' to 3' direction.

*Primers were designed and reported by Larson et al. 2007.

Supplementary Table S3. Singleplex PCR components used in Kiel for mtDNA analysis

Component	Volume/concentration
$MgCl_2$ 50 mM	0.75 µl
10 x buffer	2.5 µl
dNTPs	2 µl/each 200 µmol dNTP
Taq polymerase (5 U/µl)	0.2 µl
Primer_f	0.75 µl / 0.4 µM
Primer_r	0.75 µl / 0.4 µM
DMSO	1 µl
DNA extract	1-5 µl
ddH_2O	12.05 –16.05 µl

Supplementary Table S4. Mutations in the *MC1R* gene causing coat color variation

Codon	**4**	**17**	**21**	**22**	**102**	**117**	**121**	**122**	**124a**	**124b**	**164**	**166**	**243**	**301**
Wild-type	T	G	G	-	T	G	T	G	C	G	C	C	G	C
Mutation and the associated *MC1R*-genotype	C 103	A 104/105/201/202/203	A 502	CC 501/502/503	C 201/202/203	A 105	C 102/103/104/105/201/202/203	A 202	T 104/203	A 301/501/502/503	T 401/503	T 503	A 401	T 104/105

Nomenclature follows Fang et al. 2009.

Supplementary Table S5. Primers used to amplify six fragments of the *MC1R* gene

Set	**Primer name**	**Sequence**	**Fragment size**
MC1R1	MC1R_1f	CACCTCTGGGAGCCATGA	171 bp
	MC1R_1r	CGTCTGGTTGGTCTGGTTG	
MC1R2	MC1R_2f	ACCTGCTGGTGAGCGTGAG	150 bp
	MC1R_2r	AGCAGAGGCTGGACACCAT	
MC1R3	MC1R_3f	CGCTACCACAGCATCGTG	120 bp
	MC1R_3r	GATGAAGAGGGTGCTGGAGA	
MC1R4	MC1R_4f	GCGGTACTGTACGTCCACAT	154 bp
	MC1R_4r	CCCAGCAGAGGAGGAAGAC	
MC1R5	MC1R_5f	CTCCACAAGACGCAGCAC	94 bp
	MC1R_5r	CCCAGCAGAGGAGGAAGAC	
MC1R6	MC1R_6f	TCGTCATCTGCAACTCCATC	90 bp
	MC1R_6r	AGCACTGCAGCACCTCCT	

All primers are listed 5' to 3'.

Supplementary Table S6. Singleplex and multiplex PCR components used for *MC1R* analysis

Component	Volume/concentration	
	singleplex	**multiplex**
$MgCl_2$ 50 mM	0.75 µl	0.75 µl
10 x buffer	2.5 µl	2.5 µl
dNTPs	2 µl/each 200 µmol dATP, dCTRP, dTTP, 150 µmol dc7-GTP and 50 µmol GTP	2 µl
Taq polymerase (5 U/µl)	0.2 µl	0.2 µl
Primer_f	0.75 µl / 0.4 µM	each 0.75 µl / 0.4 µM
Primer_r	0.75 µl / 0.4 µM	each 0.75 µl / 0.4 µM
DMSO	1 µl	1 µl
DNA extract	1-5 µl	1-5 µl
ddH_2O	12.05 –16.05 µl	4.55 –8.55 µl

Supplementary Table S7. SBE multiplex primers used for *MC1R* analysis, amplicon sizes and variants

	SBE primer name*	**Sequence**	**Fragment size**	**Wild-type**	**Mutation**
Multiplex 1	21	CTCCGCRCCCCCAGCC	16	G	A
	121	CARCAGCTGGACAA	14	T	C
	117	GACTGACTGACTCAGGCCGCCGTGGTGCA	29	G	A
	4	GACTGACTGACTGGGACGATGCCCGTGCT	29	T	C
	124A	GACTGACTGACTGACTGACTGACTCGCAGATGAGCAC	37	G	A
	124B	GACTGACTGACTGACTGACTGACTCGCAGATGAGCACRT	39	C	T
	166	GACTGACTGACTGACTGACTGACTGACTGATGGCCGCGATGGCCC	45	C	T
	301	GACTGACTGACTGACTGACTGACTGACTGACTGACTTGGACCCCCTCATCTA	48	C	T
Multiplex 2	22	CCCAGCCRCCCCCCG	15+17	-	+CC
	17	GGGGGYGGCTGGGGG	15	G	A
	102	GACTGACTGACTGAGACGGCCGTGCTGC	28	T	C
	122	AAAAAAAAAAAAAAAAAAAACARCAGCTGGACAAY	35	G	A
	164	GACTGACTGACTGACTGACTGACTGTGACGCTGCCCCGCG	40	C	T
	243	GACTGACTGACTGACTGACTGACTGACTTGCGGCCTCAAGGGC	43	G	A

*SBE primer name corresponds to codon number.

Supplementary Table S8. SBE reaction components and concentrations used for *MC1R* analysis

Multiplex 1			**Multiplex 2**			**SBE-Multiplex 1**	**SBE-Multiplex 2**
SBE primer name	µM	Volume for one sample	SBE primer name	µM	Volume for one sample		
21	0.2	0.2 µl	22	0.8	0.8 µl	5µl SNaPshot multiplex mix	5 µl SNaPshot multiplex mix
121	0.1	0.1 µl	17	0.8	0.8 µl		
117	0.8	0.8 µl	102	0.1	0.1 µl	1-3 µl cleaned multiplex-PCR product	1-3 µl cleaned multiplex PCR product
4	0.1	0.1 µl	122	0.4	0.4 µl		
124A	0.1	0.1 µl	164	0.4	0.4 µl	2 µl SBE mix	2.6 µl SBE mix
124B	0.1	0.1 µl	243	0.1	0.1 µl		
166	0.4	0.4 µl			2.6 µl	0-2 µl ddH_2O	0-2 µl ddH_2O
301	0.2	0.2 µl					
Sum		2 µl			2.6 µl	10 µl	10-10.6 µl

Supplementary Table S9. Singleplex PCR components used in Durham for mtDNA analysis

Component	Volume/concentration
Taq GOLD	1.25 U
Gold buffer	1 x
$MgCl_2$	2.5 mM
BSA (Bovine Serum Albumin)	0.5 g/µl
each dNTP	200 µM
each forward and reverse primer	0.8 µM
aDNA extract	2 µl
ddH_2O	12.05 –16.05 µl

Supplementary Table S10. Sample size of modern reference specimens for GMM and traditional metric analyses

Skeletal element	Domestic pig	Wild boar
Upper M2	59	68
Lower M2	53	73
Upper M3	40	32
Lower M3	42	33

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