

Supporting Information

Lacan et al. 10.1073/pnas.1100723108

SI Materials and Methods

Ancient DNA Procedures. Drastic precautions were taken to avoid contaminations by modern DNA templates (1): pre-PCR and post-PCR procedures were carried out in two separate laboratories located on two separate floors. Pre-PCR procedures were performed in a dedicated laboratory under laminar flux. Workbenches, surfaces, and all equipment were systematically wiped with bleach, rinsed with ultrapure water, and irradiated for at least 2 h with UV light before each manipulation. Laboratory access was limited to authorized personnel only who always wore gloves, overshoes, laboratory coats, and face masks. Pipettes, plastic ware, and aerosol-resistant tips were sterile and used exclusively for ancient DNA work. DNA from people handling the anthropological material (members of the museum and laboratory staff) was also analyzed to rule out recent contamination. DNA extracted from sheep or goat bone fragments also retrieved in the ossuary were used as a negative control to detect potential contamination that could have occurred during excavation.

Statistical Analyses. To study putative genetic relationships between individuals from the ossuary, kinship was determined from autosomal STR profiles with ML-Relate software (2) and confirmed with DNA•VIEW Software (3), with which the LR was calculated assuming a prior probability of 0.5.

Human specimens from necropoles cannot be of course considered as a population in a statistical sense. Furthermore ancient DNA data could not be obtained for all the specimens buried, and Y-haplotypes were not determined for all male individuals. However, to try to characterize affinities between the ancient Treilles specimens and current European populations, we performed cross-population comparisons from HVI sequences and partial Y-chromosomal haplotypes with the ARLEQUIN 3.1

software (4). Two databases were compiled for both uniparental markers. The mtDNA database comprises 14,699 HVI haplotypes associated with their corresponding haplogroup. The NRY database comprises 49 European populations representing 10,488 Y-STR profiles. References used to compile these databases are available in Table S8. For maternal lineages, comparisons were based on HVI haplotypes, and for paternal lineages, they were based on seven STR markers (DYS19, DYS389a, DYS389b, DYS390, DYS391, DYS393, and DYS439) and on the seven male individuals for whom complete datasets were obtained (195, 575, 584, 596, 615, 616, and 636). The pattern of genetic differentiation was visualized by multidimensional scaling plot (XLstat, version 7.5.2) and by plotting on a map all F_{ST} values obtained in the comparison between the Treilles population and each population in the database, using Surfer software (version 8.0; Golden Software).

The percentage of shared lineages between Treilles and each present-day population in the databases was graphically also plotted on a map by using Surfer software (version 8.0; Golden Software).

A haplotype network was generated for NRY haplogroup G2a* from the Treilles data and all European data via the median-joining algorithm of Network, version 4.5.1.6. To obtain the most parsimonious networks the reticulation permissivity was set to zero. Datasets were preprocessed using the star contraction option in Network, version 4.5.1.6 (5). Because of the high level of reticulation in the G2a* sample, Y-STR loci were subdivided into two mutation rate classes based on observed STR allelic variance and weighted as follows: 2 (low) for DYS391 and DYS392 and 1 (high) for DYS389I, DYS389II, DYS19, DYS393, and DYS390 (6).

1. Keyser C, et al. (2009) Ancient DNA provides new insights into the history of south Siberian Kurgan people. *Hum Genet* 126:395–410.
2. Kalinowski S, Wagner A, Taper M (2006) ML-Relate: a computer program for maximum likelihood estimation of relatedness and relationship. *Mol Ecol Notes* 6: 576–579.
3. Brenner CH (1997) Symbolic kinship program. *Genetics* 145:535–542.
4. Excoffier L, Laval G, Schneider S (2005) Arlequin (version 3.0): An integrated software package for population genetics data analysis. *Evol Bioinform Online* 1:47–50.
5. Forster P, Torroni A, Renfrew C, Röhl A (2001) Phylogenetic star contraction applied to Asian and Papuan mtDNA evolution. *Mol Biol Evol* 18:1864–1881.
6. Tishkoff SA, et al. (2007) History of click-speaking populations of Africa inferred from mtDNA and Y chromosome genetic variation. *Mol Biol Evol* 24:2180–2195.

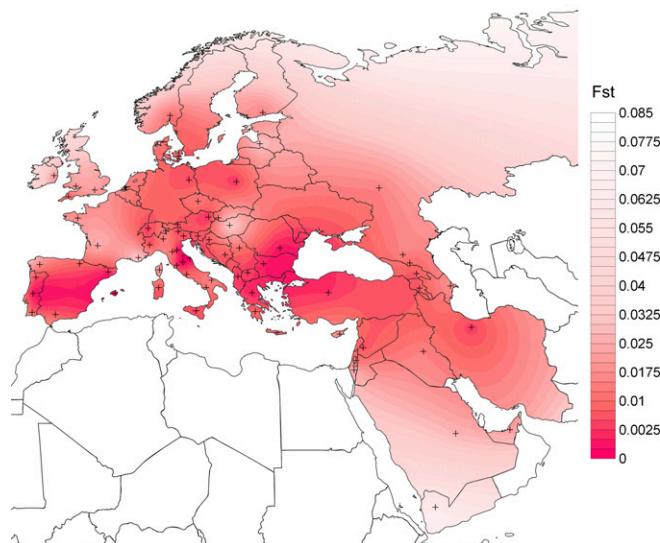


Fig. S1. Spatial distribution of the genetic matrilineal distances between Treilles samples and modern Western Eurasian populations.

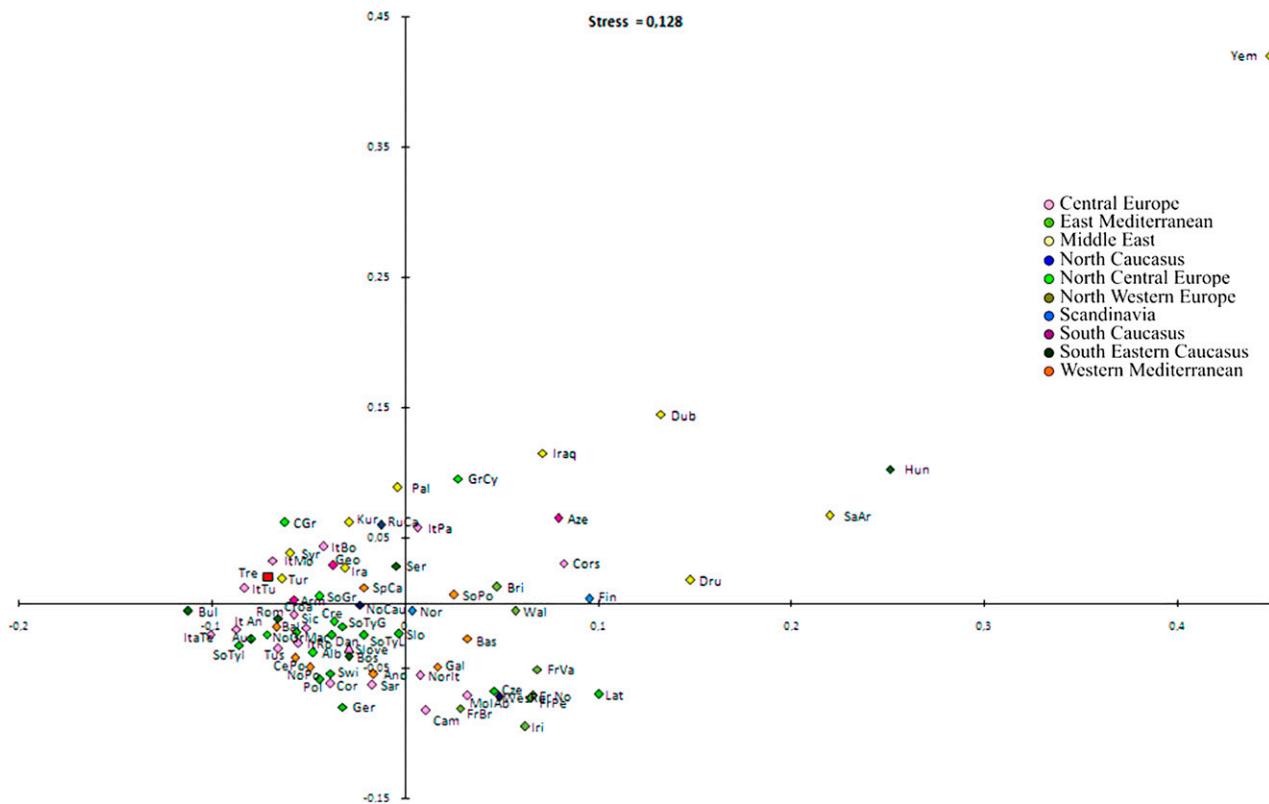


Fig. S2. Multidimensional scaling plot of genetic distances calculated for mtDNA data. The red square represents Treilles samples.

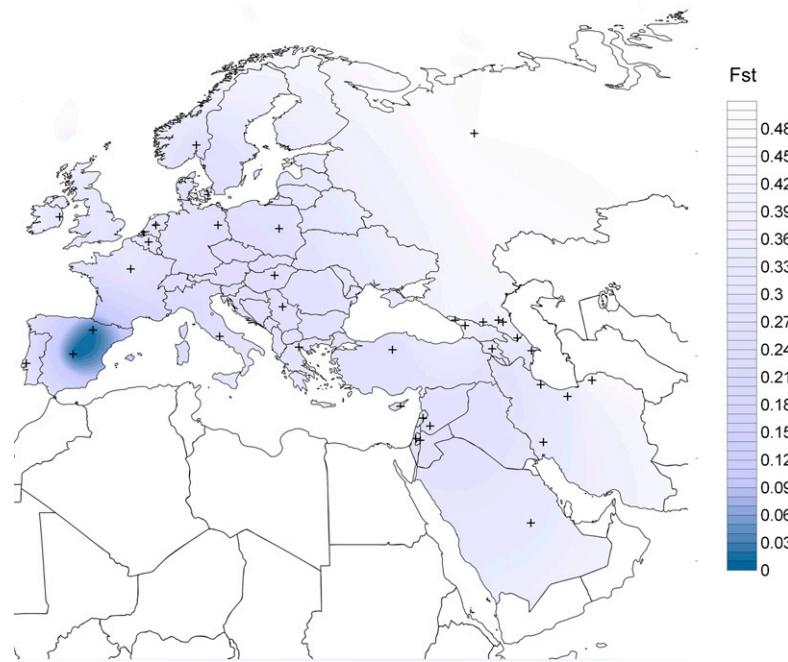


Fig. S3. Spatial distribution of the genetic patrilineal distances between Treilles male samples and modern Western Eurasian populations.

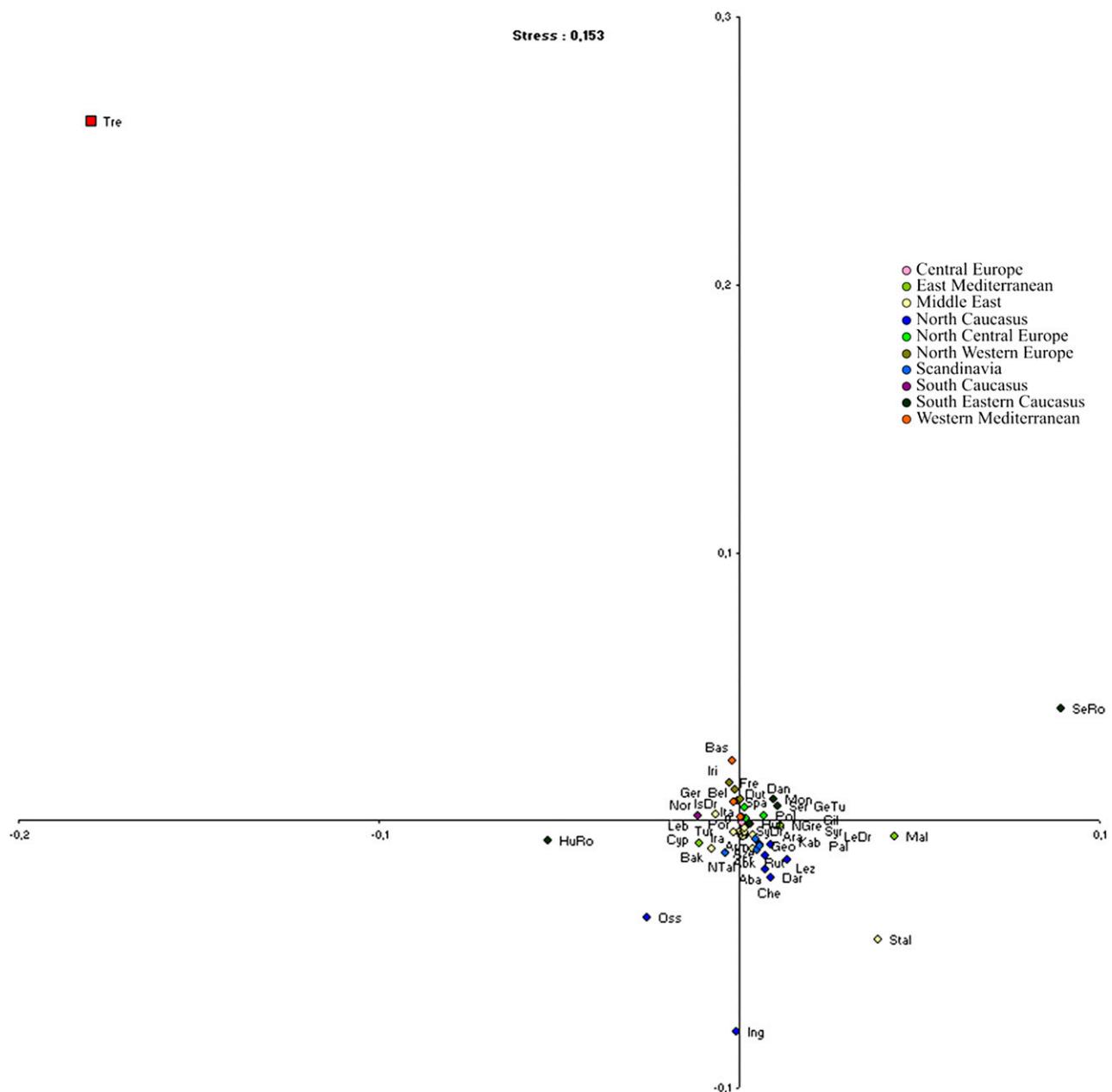


Fig. S4. Multidimensional scaling plot of genetic distances calculated for Y-chromosomal data. The red square represents Treilles samples.

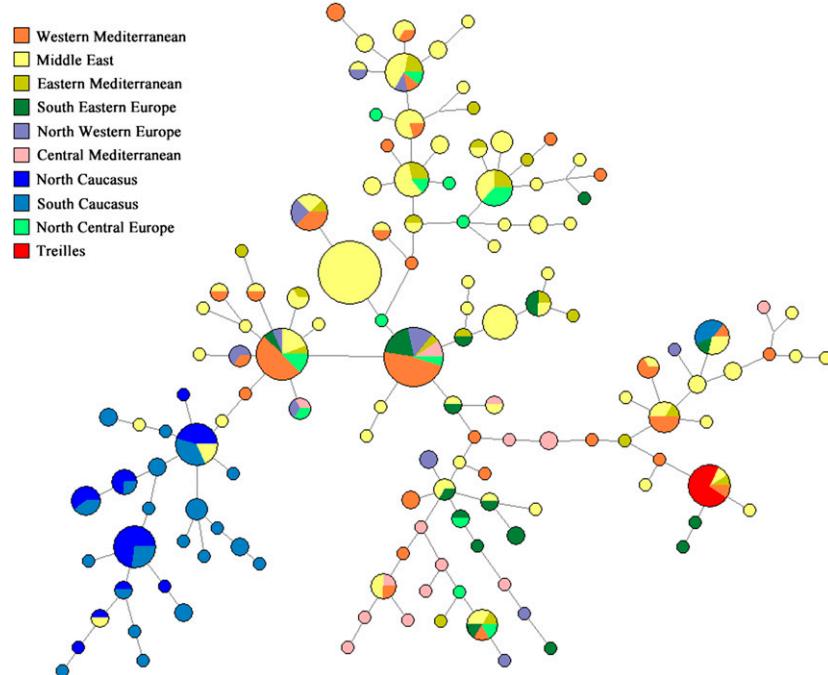


Fig. S5. Median joining network of Y-G2a haplotypes in current western European populations and in the Treilles male specimens (in red).

Table S1. Consensus STR autosomal profiles of the 24 Treilles human specimens

Sample name	Quantity, ng/ μ L	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	AMEL	D5S818	FGA	
137	6.20 $\times 10^{-3}$	(12)/13	(29)/30	(8)/12	12/12	16/17	6/6	12/12	11/12	17/(19)	12/15.2	17/17	(8/8)	12/16	X/Y	12/13	22/23	
139	5.07 $\times 10^{-3}$	(11/13)	31.2/33.2	9/9	11/11	—	—	9/10	11/12	24/25	—	(17/	—	14/15	X/Y	12/12	22/24	
195	2.59 $\times 10^{-4}$	10/14	30.2/31.2	9/12	11/11	15/17	6/9,3	8/11	9/(13)	17/19	12/14	9/(11)	(12)/14	X/Y	11/13	20/24		
209	NA	12/14	30/30	(7)/10	(9/12)	18/18	6/(8)	9/(13)	9/9	(20/20)	13/14	(15)/	(11/	13/19	X/Y	11/11	(19)/20	
570	1.78 $\times 10^{-2}$	10/14	28/31	11/12	11/(12)	18/18	—	8/8	11/11	17/21	12/13	17/20	(8/11)	(14)/17	X/Y	11/13	21/22	
573	1.91 $\times 10^{-2}$	11/14	31.2/31.2	(10/12)	9/(11)	16/17	7/7	9/(10)	(9/12)	(17/17)	14/15	14/16	(11/	16/(19)	X/X	12/12	21/23	
575	1.23 $\times 10^{-2}$	11/16	27/28	10/12	12/12	15/18	6/7	8/11	9/12	17/21	12/13	17/17	8/11	14/16	X/Y	10/11	23/24	
577	5.19 $\times 10^{-3}$	(10/10)	(29/32.2)	10/12	10/12	(16/16)	—	8/(12)	(9/11)	(21/21)	(14/14)	—	(13)/14	(X/Y)	(13/13)	24/25		
579	1.97 $\times 10^{-2}$	14/15	29/32.2	12/(13)	10/(12)	18/18	6/9,3	8/12	8/12	20/21	14/14	(15)/	8/11	12/15	X/Y	12/13	22/23	
583	7.51 $\times 10^{-3}$	14/16	28/(30)	8/(12)	10/10	(15)/18	(9/9,3)	8/11	(14/14)	17/(20)	13/15	(15)/	—	(14)/19	X/Y	(10)/12	24/24	
584	1.21 $\times 10^{-2}$	10/16	31.2/32.2	10/12	10/12	(15)/18	9/9	9/13	9/13	16/21	12/14	17/17	8/8	11/20	X/Y	11/(15)	20/24	
587	6.75 $\times 10^{-3}$	10/(13)	(24.2)/	—	(13/13)	16/16	—	8/8	—	—	13/14.2	(15/	(11/	—	X/Y	12/12	—	
588	3.38 $\times 10^{-3}$	11/14	24.2/30	11/(12)	10/10	(16)/18	9,3/	10/12	(12)/13	23/23	14/16	14/18	—	13/17	X/Y	11/12	21/24	
592	1.52 $\times 10^{-3}$	11/15	31/31.2	(10)/12	12/12	(17)/18	7/9,3	11/11	(12)/13	17/(23)	13/14	15/16	8/8	14/20	X/Y	11/12	24/24	
593	1.63 $\times 10^{-2}$	—	—	12/12	(10/10)	—	—	10/11	9/(11)	—	—	(17/	—	(12/17)	(X/Y)	—	25/26	
596	1.18 $\times 10^{-2}$	13/13	29/33.2	9/10	10/11	16/17	6/9,3	8/11	9/12	16/24	13/13	14/16	8/8	15/16	X/Y	11/12	19/25	
600	4.43 $\times 10^{-3}$	13/13	28/28	12/12	10/(11)	16/17	9/9,3	8/11	12/12	(17)/23	13/13	15/15	(8/8)	14/14	X/Y	12/12	23/25	
604	NA	10/15	29.2/31.2	8/9	10/12	18/19	(6)/8	9/11	12/13	17/(25)	15/(16)	18/19	—	18/20	X/Y	11/12	(21)/26	
611	Undet	14/14	(28/30)	—	(9/9)	14/15	9.3/	(8/11)	—	—	(13)/14	16/17	(8/8)	(12/17)	X/Y	(11/11)	(19/19)	
612	3.42 $\times 10^{-3}$	10/15	(28/28)	—	10/10	(16)/18	(9/9,3)	8/8	11/11	17/20	13/15	15/15	(8/8)	12/19	X/Y	10/12	24/24	
614	5.90 $\times 10^{-3}$	10/13	28/29	(8/10)	11/11	17/18	(7/7)	(8/8)	8/11	11/12	(23/23)	12/12	14/14	—	18/19	X/X	10/13	21/21
615	1.85 $\times 10^{-2}$	11/12	28/28	(9/11)	12/12	15/15	9/(9,3)	8/11	8/13	20/20	15/2/	14/14	11/11	12/18	X/Y	11/11	20/20	
616	3.34 $\times 10^{-2}$	10/13	28/33.2	10/11	10/12	18/18	6/9,3	8/11	11/13	17/20	13/16	15/16	8/8	19/20	X/Y	11/12	22/24	
636	2.01 $\times 10^{-2}$	10/10	(31.2)/	8/9	12/13	15/18	(6)/8	9/11	12/14	17/24	15/16	17/19	8/8	15/18	X/Y	12/12	21/21	
Research team																		
1		13/13	28/31	10/11	10/12	15/17	8/9	12/13	12/12	18/24	13/15	17/17	8/11	11/16	X/Y	11/12	21/	
2		13/14	28/29	8/10	11/11	15/18	7/9,3	11/11	11/12	24/25	13/15.2	14/17	8/10	12/15	X/Y	11/13	21/22	
3		12/14	29/29	9/11	12/12	14/18	9/9,3	12/12	11/11	17/19	13/13	15/15	11/11	14/17	X/X	11/11	21/23	
4		10/11	30/32.2	10/10	11/12	16/17	9/9,3	8/11	11/12	20/23	14/14	16/18	11/12	12/13	X/X	11/13	19/25	
5		10/13	29/30	9/11	10/11	14/18	9/9,3	11/11	11/14	17/22	14/15.2	14/18	8/12	15/17	X/Y	12/12	20/23	

Dashes denote that alleles could not be clearly amplified for the locus in question. Consensus allelic profiles were built after two amplifications performed on at least three different DNA extracts for each sample. Alleles in brackets were observed just once. The five last profiles are those of the researchers of the Natural History Museum of Toulouse (France) and of the laboratory members who have recently been in contact with the samples.

The DNA quantity mentioned was obtained from one DNA extract per sample with the Quantifiler Human DNA Quantification Kit (Applied Biosystems). Undet, undetermined; NA, data not acquired.

Table S2. MtDNA haplotypes and haplogroups inferred for each Treilles specimen

Sample Name	HVI polymorphisms	SNP typing results																		Haplotype inferred from HVI sequencing	Haplotype inferred from two SNP genotyping techniques
		U5 or K2b1	T	G	C	A	G	C	T	G	T	T	G	A	C	T	C	A	G	U5	
137	16224C	H	J	T	G	C	A	G	T	G	T	A	T	T	A	G	C	T	C	A	J1
139	16270T 16311C	U5	T	T	G	C	A	G	C	T	G	T	T	G	A	A	C	T	C	A	U5
195	16192T 16270T	U5	T	G	C	A	G	T	T	G	T	A	T	T	A	A	G	T	C	A	J1
209	16069T 16126C	J	T	G	C	A	G	T	T	G	C	T	G	T	A	A	C	T	C	A	X2
570	16189C 16223T	X2	T	G	C	A	G	T	G	C	T	G	T	A	A	C	T	C	A	A	X2
	16278T																				
571	CRS	H*	T	G	C	A	G	T	G	T	G	T	G	T	G	T	G	T	C	A	U
573	16298C	HV0	T	G	C	A	G	T	G	T	G	T	G	T	G	T	G	A	A	G	HV0
575	16227G 16256T	U5	T	G	C	A	G	T	G	T	G	T	G	T	G	T	G	A	A	G	U5
577	CRS	H?	C	G	C	A	G	T	G	T	G	T	G	T	G	C	C	T	C	A	H3
579	16224C 16270T	U5 or K2b1	T	G	C	A	G	C	T	G	T	G	T	G	T	G	A	A	C	A	U5
581	CRS	H*	C	G	C	A	G	T	G	T	G	T	G	T	G	C	C	T	C	A	H3
583	16069T 16126C	J	T	G	C	A	G	T	G	T	G	T	A	T	G	C	C	T	C	A	J1
584	16126C 16294T	T2b	T	G	C	G	A	T	T	G	T	T	G	T	G	A	A	C	T	—	T2b
	16296T 16304C																				
587	16069T 16126C	J	T	G	C	A	G	T	T	G	T	A	T	T	A	G	C	T	C	A	J1
588	16126C 16294T	T2b	—	G	C	G	A	T	T	G	T	G	T	G	A	A	C	T	—	A	T2b
592	16183C 16189C	X	T	G	C	A	G	T	T	G	C	T	G	T	A	A	C	T	C	A	X2
	16223T 16278T																				
596	16269G	H	C	G	C	A	G	T	T	G	T	A	T	C	G	A	A	C	T	C	H1
593	CRS	H*	C	G	C	A	G	T	T	G	T	A	T	C	G	A	A	C	T	C	H1
600	CRS	H*	C	G	C	A	G	T	T	G	T	A	T	C	G	A	A	C	T	C	H3
603	CRS	H*	C	G	C	A	G	T	T	G	T	A	T	C	G	A	A	C	T	C	H1
604	16224C 16311C	K	T	G	C	A	G	T	T	G	T	A	T	C	G	T	T	C	A	G	K1a
609	16298C	HV0	T	G	C	—	G	T	T	G	T	—	T	G	T	C	T	C	A	A	HV0
611	16189C 16192T	U5b1c	T	G	C	A	G	T	T	G	C	T	G	T	G	—	A	C	T	C	U5b1c
	16270T 16311C																				
612	16069T 16126C	J	T	G	C	A	G	T	T	G	T	A	T	T	A	A	G	C	T	C	J1
614	16224C 16311C	K	T	G	C	A	G	T	T	G	T	G	T	T	G	T	T	C	A	G	K1a
615	16183C 16189C	X	T	G	C	A	G	T	T	G	C	T	G	T	A	A	C	T	C	A	X2
	16223T 16278T																				
616	16069T 16126C	J	T	G	C	A	G	T	T	G	C	T	T	A	A	G	C	T	C	A	J1
636	16183C 16189C	X	T	G	C	A	G	T	T	G	C	T	T	A	A	C	T	C	A	A	X2
	16223T 16278T																				
637	16298C	HV0	T	G	C	A	G	T	T	G	C	T	T	A	G	T	T	G	A	V	
Research team																					
3	16270T	U5	T	G	C	A	G	C	T	G	T	T	G	T	T	G	T	T	C	G	U5
5	CRS	H*	C	G	C	A	G	T	T	G	T	T	G	T	C	G	A	A	C	A	H
4	16093C 16189C	U5	T	G	C	A	G	T	T	G	T	T	G	T	T	G	A	A	C	G	U5
	16270T 16274A																				
1	CRS	H*	C	G	C	A	G	T	T	G	T	T	G	T	C	G	C	T	C	A	H3
2	16129A 16223T	I	T	G	C	A	G	T	T	G	T	T	G	T	G	A	A	C	A	N15	I

Mitochondrial haplogroups were established by HV1 sequencing as well as by SNP typing of coding positions of the mtDNA. SNPs in bold are variants at concerned positions.

Table S3. F_{ST} values calculated between Treilles and modern Western Eurasian population data

Population	F_{ST}	P value
Middle East		
Iranians	0.00338	0.25225 ± 0.0353
Saudi Arabians	0.02746	0.00000 ± 0.0000
Syrians	0.00588	0.14414 ± 0.0309
Iraqis	0.01515	0.07207 ± 0.0227
Druze	0.02639	0.00000 ± 0.0000
Yemenis	0.06229	0.00000 ± 0.0000
Kurds	0.01418	0.04505 ± 0.0203
Dubai	0.02235	0.00901 ± 0.0091
Palestinians	0.01156	0.02703 ± 0.0139
Turks	0.00216	0.27027 ± 0.0303
North Caucasus		
Russian Caucasians	0.0157	0.01802 ± 0.0121
Western Russians	0.01538	0.01802 ± 0.0121
Other North Caucasus populations	0.00965	0.05405 ± 0.0201
South Caucasus		
Georgians	0.00712	0.10811 ± 0.0264
Armenians	0.00719	0.05405 ± 0.0201
Azerbaijanis	0.01911	0.01802 ± 0.0121
Northwestern Europe		
British	0.02286	0.00000 ± 0.0000
Bretagne	0.01955	0.02703 ± 0.0139
Normandie French	0.02691	0.01802 ± 0.0121
Perigord-Limousin French	0.02691	0.00000 ± 0.0000
Var French	0.03602	0.00000 ± 0.0000
Welsh	0.02329	0.00901 ± 0.0091
Cornish	0.00762	0.17117 ± 0.0286
Irish	0.02224	0.00000 ± 0.0000
North Central Europe		
Germans	0.00461	0.13514 ± 0.0365
Danish	0.00769	0.11712 ± 0.0273
Czechs	0.01481	0.03604 ± 0.0148
Polish	0.00255	0.27027 ± 0.0470
Slovakians	0.01472	0.02703 ± 0.0194
Swiss	0.00295	0.27928 ± 0.0394
Austrians	-0.00027	0.43243 ± 0.0485
Latvians	0.03072	0.00000 ± 0.0000
South Tyrol Ladins	0.01427	0.03604 ± 0.0201
South Tyrol Germans	0.00664	0.20721 ± 0.0430
South Tyrol Italians	0.00259	0.23423 ± 0.0364
Scandinavia		
Norwegians	0.01138	0.06306 ± 0.0237
Fins	0.01576	0.25225 ± 0.0353
Southeastern Europe		
Bulgarians	0.00002	0.32432 ± 0.0473
Hungarians	0.03682	0.00000 ± 0.0000
Bosnians	0.00675	0.15315 ± 0.0305
Serbiens	0.01092	0.06306 ± 0.0139
Romanian	-0.00144	0.54054 ± 0.0664
Western Mediterranean		
North Portuguese	0.00582	0.07207 ± 0.0227
Central Portuguese	-0.00126	0.53153 ± 0.0417
South Portuguese	0.00832	0.09009 ± 0.0271
Galicians	0.01786	0.02703 ± 0.0139
Spanish Catalans	-0.00049	0.43243 ± 0.0466
Andalusians	0.00766	0.11712 ± 0.0237
Balearic islanders	-0.00189	0.52252 ± 0.0297
Basques	0.00884	0.07207 ± 0.0297
Central Mediterranean		
Northeastern Italians	0.00767	0.12613 ± 0.0242
Tuscans	0.00231	0.25225 ± 0.0445
Acone Italians	-0.00272	0.57658 ± 0.0278
Bologna Italians	-0.00108	0.51351 ± 0.0526

Table S3 Cont.

Population	F_{ST}	P value
Modena Italians	0.0145	0.05405 ± 0.0201
Pavia Italians	0.01635	0.09009 ± 0.0303
Roma Italians	0.01064	0.08108 ± 0.0286
Turino Italians	0.00218	0.32432 ± 0.0546
Terni Italians	-0.00498	0.58559 ± 0.0530
Molisio-Abruzzo-puglia Italians	0.01832	0.02703 ± 0.0139
Campania Italians	0.01079	0.13514 ± 0.0311
Sicilians	0.00451	0.17117 ± 0.0212
Corsicans	0.02365	0.00000 ± 0.0000
Sardinians	0.00736	0.15315 ± 0.0273
Slovenians	0.00745	0.16216 ± 0.0353
Croatians	0.00696	0.18919 ± 0.0212
Eastern Mediterranean		
Macedonians	0.00487	0.23423 ± 0.0411
Albanians	0.0018	0.35135 ± 0.0515
Cretans	0.00892	0.13514 ± 0.0203
Cypriots	0.01888	0.02703 ± 0.0139
Northern Greek	-0.00061	0.45946 ± 0.0286
Central Greeks	0.00043	0.36036 ± 0.0664
Southern Greeks	0.00867	0.07207 ± 0.0182

F_{ST} values calculated between mtDNA for Treilles (29 samples, 13 haplotypes) and modern Western Eurasian populations data (14,699 HV1 haplotypes).

Table S4. Shared mitochondrial lineages between Treilles and modern Western Eurasian populations

Population	Shared lineages, %	
	No mismatches allowed	One mismatch allowed
Middle East		
Iranians	2,448	4,196
Saudi Arabians	1,198	2,994
Syrians	4,444	10,000
Iraqis	1,961	9,804
Druze	3,810	7,619
Yemenis	2,985	10,448
Kurds	3,448	8,621
Dubai	1,829	4,878
Palestinians	3,030	7,071
Turks	1,961	3,922
North Caucasus		
Caucasian Russians	2,970	8,911
Western Russians	2,778	6,481
Other North Caucasus populations	1,765	4,706
South Caucasus		
Georgians	2,732	5,464
Armenians	1,613	5,914
Azerbaijanis	5,556	13,889
Northwestern Europe		
British	3,896	11,688
Bretagne French	7.5	12.5
Normandie French	6.667	11,111
Perigord-Limousin French	6.667	11,111
Var French	9.091	22,727
Welsh	17,391	30,435
Cornish	16,667	29,167
Irish	2,564	6,410
North-central Europe		
Germans	2,564	4,029
Danish	2,857	5,714
Czechs	3,125	5,208
Polish	1,527	3,308
Slovakians	5,185	8,148
Swiss	4,651	8,527
Austrians	7,463	11,940
Latvians	2,941	5,882
South Tyrol Ladins	10,204	16,327
South Tyrol Germans	12,000	16,000
South Tyrol Italians	9,756	19,512
Scandinavia		
Norwegians	3,306	8,264
Finn	3,822	7,006
South Eastern Europe		
Bulgarians	12,500	29,167
Hungarians	3,623	7,246
Bosnians	3,497	6,993
Serbiens	4,348	10,870
Romanian	5,000	12,500
Western Mediterranean		
Northern Portuguese	3.681	5.521
Central Portuguese	4.070	6.395
Southern Portuguese	5.298	7.285
Galicians	5.882	12.941
Spanish Catalans	7,527	10,753
Andalusians	4,000	10,000
Balearic islanders	7,317	24,390
Basques	8,602	12,903
Central Mediterranean		
Northeastern Italians	5,357	9,821

Table S4 Cont.

Population	Shared lineages, %	
	No mismatches allowed	One mismatch allowed
Tuscans	3,139	5,381
Acone Italians	9,091	18,182
Bologna Italians	11,111	25,000
Modena Italians	6,061	24,242
Pavia Italians	11,429	20,000
Roma Italians	3,797	10,127
Turino Italians	4,444	17,778
Terni Italians	10,000	30,000
Molisio-Abruzzo-puglia Italians	4,348	8,670
Campania Italians	2,564	12,821
Sicilians	4,587	7,339
Corsicans	9,677	19,355
Sardinians	3,822	7,006
Slovenians	7,813	14,063
Croatians	8,333	16,667
Eastern Mediterranean		
Macedonians	4,242	5,455
Albanians	4,225	11,268
Cretans	5,769	10,577
Cypriots	3,333	13,333
Northern Greek	2,885	4,327
Central Greeks	14,286	28,571
Southern Greeks	2,830	5,660

Mitochondrial shared lineages between Treilles (29 samples, 13 haplotypes) and modern Western Eurasian populations (14,699 HVI haplotypes). Analyses were performed for 0 or 1 mismatch.

Table S5. Y-haplogroups inferred from Y-STR haplotypes and NRY-SNPs typing results for the male specimens

Sample name	Y-STRs												NRY SNPs typing results										Haplogroup Y	
	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS319	DYS5385	DYS5391	DYS5393	DYS5399	DYS5635	DYS5392	H4	GATA-H4	DYS437	DYS5438	DYS448	M287	P15	Y-I-M170	M438	Y-I-M201	Y-G-P37.2	
137	14	12	23	—	18	15	—	14	10	11	—	—	11	16	—	20	—	T	—	A	T	—	P15+	G2a
139	—	12	—	—	18	15	—	—	10	11	—	—	11	16	—	10	—	T	—	A	T	—	P15+	G2a
195	14	12	23	30	18	15	(13/15)	14	10	11	21	—	—	11	16	—	—	—	A	—	A	—	P15+	G2a
209	14	12	23	—	18	15	(13/15)	14	10	—	—	—	—	11	—	—	—	—	A	—	A	—	(99.9%)	(99.9%)
570	14	12	23	—	18	—	13/(15)	14	10	11	21	11	11	16	—	—	—	T	—	A	T	—	P15+	G2a
575	14	12	23	30	18	15	13/(15)	14	10	11	21	—	11	16	10	20	—	T	—	A	T	—	P15+	G2a
577	14	—	—	—	16	—	—	13	—	—	—	—	—	12	—	—	—	C	—	G	—	C	M438+P37.2+	I2a
579	14	12	23	—	18	—	13/(15)	14	10	11	21	—	11	16	10	—	—	T	—	A	—	—	P15+	G2a
583	14	—	—	—	18	—	13/(15)	14	10	11	—	—	11	16	—	—	—	A	—	A	—	—	(99.8%)	(99.8%)
584	15	12	23	30	18	15	13/15	14	10	12	21	—	11	16	—	—	—	T	—	A	T	—	P15+	G2a
587	14	12	23	—	—	—	13/(15)	14	15	14	—	21	—	—	—	—	—	T	—	A	—	—	P15+	G2a
588	14	12	23	—	18	—	13/(15)	14	10	11	—	—	21	—	—	—	—	T	—	A	—	—	P15+	G2a
592	14	12	23	—	18	—	13/15	14	10	11	—	—	11	16	—	—	—	T	—	A	—	—	P15+	G2a
593	14	—	—	—	18	—	—	—	—	—	—	—	—	—	—	—	—	T	—	A	—	—	P15+	G2a
596	14	13	23	28	16	16	12	13	10	12	22	11	12	15	10	22	—	C	—	G	—	C	M438+P37.2+	I2a
600	14	12	—	30	18	—	13/15	14	10	11	21	—	11	16	10	—	—	T	—	A	—	—	P15+	G2a
604	14	—	—	—	18	15	—	14	10	—	21	—	11	—	—	—	—	T	—	A	—	—	P15+	G2a
611	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	T	—	A	—	—	P15+	G2a
612	14	12	—	—	18	—	(13/15)	14	10	11	21	—	11	—	—	—	—	T	—	—	—	—	G2a	G2a
615	14	12	23	30	18	15	13/15	14	10	11	21	11	11	16	10	20	—	—	A	—	T	—	(100%)	G2a
616	14	12	23	30	18	15	13/15	14	10	11	21	11	11	16	10	20	—	T	—	A	—	—	P15+	G2a
636	14	12	23	30	18	15	13/15	14	10	11	21	11	11	16	9	—	—	T	—	A	—	—	P15+	G2a
Research team	1	15	14	24	30	18	13	11/12	13	9	10	21	11	14	10	20	A	C	A	A	A	T	T	
	2	16	13	24	28	17	14	11/12	13	11	13	24	13	11	15	12	20	A	C	A	A	A	T	R1b
	5	15	14	24	30	18	14	12/14	13	11	11	24	13	12	15	12	19	A	C	A	A	A	T	R1b

Dashes denote that alleles could not be clearly amplified for the locus in question. Consensus Y-STR profiles were built after two amplifications from at least three different DNA extracts for each sample. Alleles in brackets were observed just once. The three last profiles are those of the male researchers of the Natural History Museum of Toulouse (France) and of the laboratory members who have recently been in contact with the samples. For samples 209, 583, 615, for which the Y haplogroup could not be confirmed by the typing of SNP, the determination of the haplogroup was conducted solely from the haplotype. The percentage of probability is shown in the last column. SNPs in bold are variants at concerned positions.

Table S6. F_{ST} values calculated between Y-chromosomal data of Treilles' samples and modern Western Eurasian population data (49 populations representing 10,488 Y-STR profiles)

Population	F_{ST}	P value
Middle East		
Iranians	0.29758	0.00000 ± 0.0000
Bakhtiari	0.32066	0.00000 ± 0.0000
Gilaki	0.32231	0.00000 ± 0.0000
Mazandarani	0.32759	0.00000 ± 0.0000
Syrians	0.28712	0.00000 ± 0.0000
Druze	0.28894	0.00000 ± 0.0000
Palestinians	0.27848	0.00000 ± 0.0000
Lebanese	0.27520	0.00000 ± 0.0000
Turks	0.26764	0.00000 ± 0.0000
North Caucasus		
Abazinians	0.42472	0.00000 ± 0.0000
Abkhazians	0.44302	0.00000 ± 0.0000
Chechenians	0.42307	0.00000 ± 0.0000
Darginians	0.39692	0.00000 ± 0.0000
Ingushians	0.45255	0.00000 ± 0.0000
Kabardinians	0.31682	0.00000 ± 0.0000
South Caucasus		
Georgians	0.30749	0.00000 ± 0.0000
Armenians	0.29941	0.00000 ± 0.0000
Azerbaijanis	0.31764	0.00000 ± 0.0000
Lezginians	0.40088	0.00000 ± 0.0000
Ossetians	0.35485	0.00000 ± 0.0000
Northwestern Europe		
French	0.32143	0.00000 ± 0.0000
Irish	0.28895	0.00000 ± 0.0000
Belgians	0.28996	0.00000 ± 0.0000
Dutch	0.30891	0.00000 ± 0.0000
North central Europe		
Germans	0.26655	0.00000 ± 0.0000
Danish	0.27898	0.00000 ± 0.0000
Polish	0.27598	0.00000 ± 0.0000
Scandinavia		
Norwegians	0.26608	0.00000 ± 0.0000
Southeastern Europe		
Hungarian	0.26761	0.00000 ± 0.0000
Serbian	0.28178	0.00000 ± 0.0000
Serbian Romanian		
Montenegrin	0.27567	0.00000 ± 0.0000
Western Mediterranean		
Portuguese	0.27854	0.00000 ± 0.0000
Spanish	0.00724	0.00000 ± 0.0000
Basque	0.01392	0.00000 ± 0.0000
Central Mediterranean		
Italians	0.26635	0.00000 ± 0.0000
Eastern Mediterranean		
Maltese	0.37106	0.00000 ± 0.0000
Cypriots	0.29806	0.00000 ± 0.0000
Northern Greeks	0.28846	0.00000 ± 0.0000

Table S7. Shared Y-lineages between Treilles and modern Western Eurasian populations (49 populations representing 10,488 Y-STR profiles)

Population	Shared lineages, %
Middle East	
Iranians	0
Syrians	0
Druze	0
Palestinians	0
Lebanese	0.355
Turks	0.699
North Caucasus	
Other North Caucasus populations	0
South Caucasus	
Georgians	0
Armenians	0
Azerbaijanis	0
Other South Caucasus populations	0
Northwestern Europe	
French	0
Irish	0
Belgians	0
Dutch	0
North Central Europe	
Germans	0.226
Danish	0
Polish	0
Scandinavia	
Norwegians	0
Southeastern Europe	
Hungarians	0
Serbians	0
Serbian Romanians	0
Montenegrins	0
Western Mediterranean	
Portuguese	1.980
Galician	0
Catalan	0
Other Spanish	0.248
Basque	0
Central Mediterranean	
Italians	0.385
Sicilians	0
Sardinians	0
Eastern Mediterranean	
Maltese	0
Cypriots	2.062
North Greeks	0

Table S8. References of the populations included in the databases

Population (size)	References HVS-I	Population (size)	References Y-STR
Middle East (<i>n</i> = 2,689)		Middle East (<i>n</i> = 2,482)	
Iranians	1, 2	Iranians	3
Saudi Arabians	4–6	Syrians	8
Syrians	2, 7	Druze	11
Iraqis	9		
Druze	10, 11	Palestinians	8
Yemenis	12	Lebanese	15
Kurds	2, 13	Turks	21, 22
Dubai	14		
Palestinians	2	North Caucasus (<i>n</i> = 78)	
Turks	2, 16–20	Other North Caucasus populations	26
North Caucasus (<i>n</i> = 594)		South Caucasus (<i>n</i> = 424)	
Caucasian Russians	2	Georgians	26
Western Russians	23	Armenians	26
Other North Caucasus populations	10, 19, 24, 25	Azerbaijanis	3, 26
South Caucasus (<i>n</i> = 652)		Other South Caucasus populations	26
Georgians	13, 19, 27, 28		
Armenians	2, 27, 29		
Azerbaijanis	27		
Northwestern Europe (<i>n</i> = 783)		Northwestern Europe (<i>n</i> = 408)	
British	30	French	32
French	31		
Welsh	20	Irish	34
Cornish	20	Belgians	35
Irish	20, 33	Dutch	36
North-Central Europe (<i>n</i> = 3,239)		North-Central Europe (<i>n</i> = 1,695)	
Germans	20, 23, 37–39	Germans	36, 40
Danish	2, 20	Danish	41
Czechs	42		
Polish	23, 43, 44	Polish	45
Slovakians	29, 46		
Swiss	20, 47, 48		
Latvians	49	Scandinavia (<i>n</i> = 1,967)	
Austrians	50	Norwegians	54
South Tyrol Ladins	51, 52		
South Tyrol Germans	51		
South Tyrol Italians	51		
Scandinavia (<i>n</i> = 712)			
Norwegians	53		
Finns	55–57		
Southeastern Europe (<i>n</i> = 909)		Southeastern Europe (<i>n</i> = 1,078)	
Bulgarians	16	Hungarians	61
Hungarians	58–60		
Bosnians	62, 63	Serbs	64
Serbs	62	Serbian Romanians	66
Romanian	65	Montenegrins	64
Western Mediterranean (<i>n</i> = 1,625)		Western Mediterranean (<i>n</i> = 1,442)	
Portuguese	67, 68	Portuguese	69
Galicians	68, 70	Galicians	69, 71
Spanish Catalans	72, 73	Spanish Catalans	69
Andalusians	72, 74, 75		
Balearic islanders	75		
		Other Spanish	69, 71, 76, 77
Basques	2, 72, 78–80	Basques	69
Central Mediterranean (<i>n</i> = 2,040)		Central Mediterranean (<i>n</i> = 562)	
Northeastern Italians	52, 81–84	Northern Italians	85

Table S8 Cont.

Population (size)	References HVS-I	Population (size)	References Y-STR
Tuscanians	75, 86, 87		
Other Italians: Acone, Bologna, Firenze, Modena, Pavia, Roma, Turino, Terni, Molisio- Abruzzo-puglia, Campania	84, 88, 89		
Sicilians	88, 90	Southern Italians	71
Corsicans	92	Sicilians	71, 91
Sardinians	20, 75, 93, 94	Sardinians	95
Slovenians	63		
Croatians	62		
Eastern Mediterranean (<i>n</i> = 1,298)		Eastern Mediterranean (<i>n</i> = 404)	
Macedonians	65, 88, 96, 97		
Albanians	65, 98		
Cretans	7, 88, 99	Maltese	8
Cypriots	100	Cypriots	8
Northern Greek	97, 100	Northern Greeks	101
Central Greeks	88, 97		
Southern Greeks	83, 88, 97		
Other Greeks	65		

1. Metspalu M, et al. (2004) Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. *BMC Genet* 5:26.
2. Richards M, et al. (2000) Tracing European founder lineages in the Near Eastern mtDNA pool. *Am J Hum Genet* 67:1251–1276.
3. Roewer L, Willuweit S, Stoneking M, Nasidze I (2009) A Y-STR database of Iranian and Azerbaijani minority populations. *Forensic Sci Int Genet* 4:e53–e55.
4. Abu-Amero KK, González AM, Larruga JM, Bosley TM, Cabrera VM (2007) Eurasian and African mitochondrial DNA influences in the Saudi Arabian population. *BMC Evol Biol* 7:32.
5. Abu-Amero KK, Larruga JM, Cabrera VM, González AM (2008) Mitochondrial DNA structure in the Arabian Peninsula. *BMC Evol Biol* 8:45.
6. Di Rienzo A, Wilson AC (1991) Branching pattern in the evolutionary tree for human mitochondrial DNA. *Proc Natl Acad Sci USA* 88:1597–1601.
7. Veronesi C, et al. (2001) Genetic characterization of the body attributed to the evangelist Luke. *Proc Natl Acad Sci USA* 98:13460–13463.
8. Zalloua PA, et al.; Genographic Consortium Identifying genetic traces of historical expansions: Phoenician footprints in the Mediterranean. *Am J Hum Genet* 83:633–642.
9. Al-Zahery N, et al. (2003) Y-chromosome and mtDNA polymorphisms in Iraq, a crossroad of the early human dispersals and of post-Neolithic migrations. *Mol Phylogenet Evol* 28: 458–472.
10. Macaulay V, et al. (1999) The emerging tree of West Eurasian mtDNAs: A synthesis of control-region sequences and RFLPs. *Am J Hum Genet* 64:232–249.
11. Shlush LI, et al. (2008) The Druze: A population genetic refugium of the Near East. *PLOS ONE* 3:e2105.
12. Kivisild T, et al. (2004) Ethiopian mitochondrial DNA heritage: tracking gene flow across and around the gate of tears. *Am J Hum Genet* 75:752–770.
13. Comas D, Calafell F, Bendukidze N, Fañanás L, Bertranpetti J (2000) Georgian and kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. *Am J Phys Anthropol* 112:5–16.
14. Alshamali F, Brandstätter A, Zimmermann B, Parson W (2008) Mitochondrial DNA control region variation in Dubai, United Arab Emirates. *Forensic Sci Int Genet* 2:e9–e10.
15. Zalloua PA, et al.; Genographic Consortium (2008) Y-chromosomal diversity in Lebanon is structured by recent historical events. *Am J Hum Genet* 82:873–882.
16. Calafell F, Underhill P, Tolun A, Angelicheva D, Kalaydjieva L (1996) From Asia to Europe: Mitochondrial DNA sequence variability in Bulgarians and Turks. *Ann Hum Genet* 60:35–49.
17. Comas D, Calafell F, Mateu E, Pérez-Lezaun A, Bertranpetti J (1996) Geographic variation in human mitochondrial DNA control region sequence: the population history of Turkey and its relationship to the European populations. *Mol Biol Evol* 13:1067–1077.
18. Di Benedetto G, et al. (2001) DNA diversity and population admixture in Anatolia. *Am J Phys Anthropol* 115:144–156.
19. Quintana-Murci L, et al. (2004) Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. *Am J Hum Genet* 74:827–845.
20. Richards M, et al. (1996) Paleolithic and neolithic lineages in the European mitochondrial gene pool. *Am J Hum Genet* 59:185–203.
21. Alakoc YD, et al. (2010) Y-chromosome and autosomal STR diversity in four proximate settlements in Central Anatolia. *Forensic Sci Int Genet* 4:e135–e137.
22. Cinnioğlu C, et al. (2004) Excavating Y-chromosome haplotype strata in Anatolia. *Hum Genet* 114:127–148.
23. Malyarchuk BA, et al. (2002) Mitochondrial DNA variability in Poles and Russians. *Ann Hum Genet* 66:261–283.
24. Nasidze I, et al. (2004) Mitochondrial DNA and Y-chromosome variation in the caucasus. *Ann Hum Genet* 68:205–221.
25. Lebedeva IA, Seryogin YA, Poltarau AB, *Mitochondrial DNA Polymorphism in Adygeis*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers AF285277–AF285384.
26. Nasidze I, Schädlich H, Stoneking M (2003) Haplotypes from the Caucasus, Turkey and Iran for nine Y-STR loci. *Forensic Sci Int* 137:85–93.
27. Nasidze I, et al. (2004) Genetic evidence concerning the origins of South and North Ossetians. *Ann Hum Genet* 68:588–599.
28. Reidla M, *Mitochondrial DNA Lineages in Georgia*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers AJ389196–AJ389375.
29. Metspalu E, Kivisild T, Kaldma K, Reidla M, Villems R, *Mitochondrial DNA Lineages and the History of the Roma (Gypsies)*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers AJ233203–AJ233348 and AJ240164–AJ240248 (Armenians and Slovaks).
30. Piercy R, Sullivan KM, Benson N, Gill P (1993) The application of mitochondrial DNA typing to the study of white Caucasian genetic identification. *Int J Legal Med* 106:85–90.
31. Dubut V, et al. (2004) mtDNA polymorphisms in five French groups: Importance of regional sampling. *Eur J Hum Genet* 12:293–300.
32. Balaresque P, et al. (2010) A predominantly neolithic origin for European paternal lineages. *PLoS Biol*, 10.1371/journal.pbio.1000285.
33. McEvoy B, Richards M, Forster P, Bradley DG (2004) The Longue Durée of genetic ancestry: Multiple genetic marker systems and Celtic origins on the Atlantic facade of Europe. *Am J Hum Genet* 75:693–702.
34. Ballard DJ, Phillips C, Thacker CR, Court DS (2006) Y chromosome STR haplotype data for an Irish population. *Forensic Sci Int* 161:64–68.
35. De Maesschalck K, et al. (2005) Y-chromosomal STR haplotypes in a Belgian population sample and identification of a micro-variant with a flanking site mutation at DYS19. *Forensic Sci Int* 152:89–94.
36. Rodig H, et al. (2008) Evaluation of haplotype discrimination capacity of 35 Y-chromosomal short tandem repeat loci. *Forensic Sci Int* 174:182–188.
37. Brandstätter A, Klein R, Duftnér N, Wiegand P, Parson W (2006) Application of a quasi-median network analysis for the visualization of character conflicts to a population sample of mitochondrial DNA control region sequences from southern Germany (Ulm). *Int J Legal Med* 120:310–314.
38. Lutz S, Weisser HJ, Heizmann J, Pollak S (1998) Location and frequency of polymorphic positions in the mtDNA control region of individuals from Germany. *Int J Legal Med* 111:67–77.
39. Tetzlaff S, Brandstätter A, Wegener R, Parson W, Weirich V (2007) Mitochondrial DNA population data of HVS-I and HVS-II sequences from a northeast German sample. *Forensic Sci Int* 172:218–224.
40. Hohoff C, et al. (2007) Y-chromosomal microsatellite mutation rates in a population sample from northwestern Germany. *Int J Legal Med* 121:359–363.
41. Hallenberg C, Nielsen K, Simonsen B, Sanchez J, Morling N (2005) Y-chromosome STR haplotypes in Danes. *Forensic Sci Int* 155:205–210.

42. Malyarchuk BA, Vanecek T, Derenko MV, Sip M (2006) Mitochondrial DNA variability in the Czech population, with application to the ethnic history of Slavs. *Hum Biol* 78: 681–696.
43. Grzybowski T, et al. (2007) Complex interactions of the Eastern and Western Slavic populations with other European groups as revealed by mitochondrial DNA analysis. *Forensic Sci Int Genet* 1:141–147.
44. Malyarchuk BA, Rogozin IB, Berikov VB, Derenko MV (2002) Analysis of phylogenetically reconstructed mutational spectra in human mitochondrial DNA control region. *Hum Genet* 111:46–53.
45. Rebala K, Szczercowska Z (2005) Polish population study on Y chromosome haplotypes defined by 18 STR loci. *Int J Legal Med* 119:303–305.
46. Malyarchuk BA, et al. (2008) Mitochondrial DNA variability in Slovaks, with application to the Roma origin. *Ann Hum Genet* 72:228–240.
47. Dímo-Simonin N, Grange F, Taroni F, Brandt-Casadevall C, Mangin P (2000) Forensic evaluation of mtDNA in a population from south west Switzerland. *Int J Legal Med* 113:89–97.
48. Pult I, et al. (1994) Mitochondrial DNA sequences from Switzerland reveal striking homogeneity of European populations. *Biol Chem Hoppe Seyler* 375:837–840.
49. Pliss L, et al. (2006) Mitochondrial DNA portrait of Latvians: towards the understanding of the genetic structure of Baltic-speaking populations. *Ann Hum Genet* 70:439–458.
50. Parson W, Parsons TJ, Scheithauer R, Holland MM (1998) Population data for 101 Austrian Caucasian mitochondrial DNA d-loop sequences: Application of mtDNA sequence analysis to a forensic case. *Int J Legal Med* 111:124–132.
51. Thomas MG, et al. (2008) New genetic evidence supports isolation and drift in the Ladin communities of the South Tyrolean Alps but not an ancient origin in the Middle East. *Eur J Hum Genet* 16:124–134.
52. Vernesi C, Fuselli S, Castri L, Bertorelle G, Barbujani G (2002) Mitochondrial diversity in linguistic isolates of the Alps: a reappraisal. *Hum Biol* 74:725–730.
53. Helgason A, et al. (2001) mtDNA and the islands of the North Atlantic: Estimating the proportions of Norse and Gaelic ancestry. *Am J Hum Genet* 68:723–737.
54. Dupuy BM, et al. (2001) Y-chromosome variation in a Norwegian population sample. *Forensic Sci Int* 117:163–173.
55. Kittles RA, et al. (1999) Autosomal, mitochondrial, and Y chromosome DNA variation in Finland: evidence for a male-specific bottleneck. *Am J Phys Anthropol* 108:381–399.
56. Lahermo P, et al. (1996) The genetic relationship between the Finns and the Finnish Saami (Lapps): Analysis of nuclear DNA and mtDNA. *Am J Hum Genet* 58:1309–1322.
57. Meinilä M, Finnilä S, Majamaa K (2001) Evidence for mtDNA admixture between the Finns and the Saami. *Hum Hered* 52:160–170.
58. Bogács-Szabó E, et al. (2005) Mitochondrial DNA of ancient Cumans: Culturally Asian steppe nomadic immigrants with substantially more western Eurasian mitochondrial DNA lineages. *Hum Biol* 77:639–662.
59. Irwin J, et al. (2007) Hungarian mtDNA population databases from Budapest and the Baranya county Roma. *Int J Legal Med* 121:377–383.
60. Tömöry G, et al. (2007) Comparison of maternal lineage and biogeographic analyses of ancient and modern Hungarian populations. *Am J Phys Anthropol* 134:354–368.
61. Völgyi A, Zalán A, Szvetnik E, Pamjav H (2009) Hungarian population data for 11 Y-STR and 49 Y-SNP markers. *Forensic Sci Int Genet* 3:e27–e28.
62. Harvey M, Gordon K, Owens K, Lee M, King MC, *MtDNA Sequences from Balkan Populations*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers AY005666–AY005724 (Croatians), AY005729–AY005784 (Serbians), and AY005485–AY005644 (Bosnians).
63. Malyarchuk BA, et al. (2003) Mitochondrial DNA variability in Bosnians and Slovenians. *Ann Hum Genet* 67:412–425.
64. Mirabal S, et al. (2010) Human Y-chromosome short tandem repeats: A tale of acculturation and migrations as mechanisms for the diffusion of agriculture in the Balkan Peninsula. *Am J Phys Anthropol* 142:380–390.
65. Bosch E, et al. (2006) Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. *Ann Hum Genet* 70: 459–487.
66. Regueiro M, et al. (2011) Divergent patrilineal signals in three Roma populations. *Am J Phys Anthropol* 144:80–91.
67. Pereira L, Cunha C, Amorim A (2004) Predicting sampling saturation of mtDNA haplotypes: An application to an enlarged Portuguese database. *Int J Legal Med* 118:132–136.
68. González AM, et al. (2003) Mitochondrial DNA affinities at the Atlantic fringe of Europe. *Am J Phys Anthropol* 120:391–404.
69. Adams SM, et al. (2008) The genetic legacy of religious diversity and intolerance: Paternal lineages of Christians, Jews, and Muslims in the Iberian Peninsula. *Am J Hum Genet* 83: 725–736.
70. Salas A, Comas D, Lareu MV, Bertranpetti J, Carracedo A (1998) mtDNA analysis of the Galician population: A genetic edge of European variation. *Eur J Hum Genet* 6:365–375.
71. Rodríguez V, et al. (2009) Genetic sub-structure in western Mediterranean populations revealed by 12 Y-chromosome STR loci. *Int J Legal Med* 123:137–141.
72. Córte-Real HB, et al. (1996) Genetic diversity in the Iberian Peninsula determined from mitochondrial sequence analysis. *Ann Hum Genet* 60:331–350.
73. Crespillo M, et al. (2000) Mitochondrial DNA sequences for 118 individuals from northeastern Spain. *Int J Legal Med* 114:130–132.
74. Casas MJ, Hagelberg E, Freigal R, Larruga JM, González AM (2006) Human mitochondrial DNA diversity in an archaeological site in al-Andalus: Genetic impact of migrations from North Africa in medieval Spain. *Am J Phys Anthropol* 131:539–551.
75. Falchi A, et al. (2006) Genetic history of some western Mediterranean human isolates through mtDNA HVR1 polymorphisms. *J Hum Genet* 51:9–14.
76. Gaibar M, et al. (2010) STR genetic diversity in a Mediterranean population from the south of the Iberian Peninsula. *Ann Hum Biol* 37:253–266.
77. Flores C, et al. (2003) A predominant European ancestry of paternal lineages from Canary Islanders. *Ann Hum Genet* 67:138–152.
78. Alfonso-Sánchez MA, et al. (2008) Mitochondrial DNA haplogroup diversity in Basques: A reassessment based on HV1 and HVII polymorphisms. *Am J Hum Biol* 20:154–164.
79. Alzualde A, Izagirre N, Alonso S, Alonso A, de la Rúa C (2005) Temporal mitochondrial DNA variation in the Basque Country: Influence of post-neolithic events. *Ann Hum Genet* 69: 665–679.
80. Bertranpetti J, et al. (1995) Human mitochondrial DNA variation and the origin of Basques. *Ann Hum Genet* 59:63–81.
81. Guimaraes S, et al. (2009) Genealogical discontinuities among Etruscan, Medieval, and contemporary Tuscans. *Mol Biol Evol* 26:2157–2166.
82. Mogentale-Profizi N, et al. (2001) Mitochondrial DNA sequence diversity in two groups of Italian Veneto speakers from Veneto. *Ann Hum Genet* 65:153–166.
83. Vernesi C, et al. (2004) The Etruscans: A population-genetic study. *Am J Hum Genet* 74:694–704.
84. Babalini C, et al. (2005) The population history of the Croatian linguistic minority of Molise (southern Italy): A maternal view. *Eur J Hum Genet* 13:902–912.
85. Turrina S, Atzei R, De Leo D (2006) Y-chromosomal STR haplotypes in a Northeast Italian population sample using 17plex loci PCR assay. *Int J Legal Med* 120:56–59.
86. Achilli A, et al. (2007) Mitochondrial DNA variation of modern Tuscans supports the near eastern origin of Etruscans. *Am J Hum Genet* 80:759–768.
87. Francalacci P, Bertranpetti J, Calafell F, Underhill PA (1996) Sequence diversity of the control region of mitochondrial DNA in Tuscany and its implications for the peopling of Europe. *Am J Phys Anthropol* 100:443–460.
88. Forster P, et al. (2002) Continental and subcontinental distributions of mtDNA control region types. *Int J Legal Med* 116:99–108.
89. Turchi C, et al.; Ge.F.I. Group Italian mitochondrial DNA database: results of a collaborative exercise and proficiency testing. *Int J Legal Med* 122:199–204.
90. Cali F, et al. (2001) MtDNA control region and RFLP data for Sicily and France. *Int J Legal Med* 114:229–231.
91. Di Gaetano C, et al. (2009) Differential Greek and northern African migrations to Sicily are supported by genetic evidence from the Y chromosome. *Eur J Hum Genet* 17:91–99.
92. Varesi L, et al. (2000) Mitochondrial control-region sequence variation in the Corsican population, France. *Am J Hum Biol* 12:339–351.
93. Caramelli D, et al. (2007) Genetic variation in prehistoric Sardinia. *Hum Genet* 122:327–336.
94. Varesi L, Piras IS, Calo CM, Vona G, *Mitochondrial DNA Polymorphism in the HVRI Control Region in the Population of Sardinia (Gallura)*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers DQ081414–DQ081464.
95. Ghiani ME, et al. (2009) Population data for Y-chromosome haplotypes defined by AmpFISTR YFiler PCR amplification kit in North Sardinia (Italy). *Coll Antropol* 33:643–651.
96. Zimmermann B, et al. (2007) Mitochondrial DNA control region population data from Macedonia. *Forensic Sci Int Genet* 1:e4–e9.
97. Kouvatzi A, Karaïskou N, Apostolidis A, Kirmizidis G (2001) Mitochondrial DNA sequence variation in Greeks. *Hum Biol* 73:855–869.
98. Belledi M, et al. (2000) Maternal and paternal lineages in Albania and the genetic structure of Indo-European populations. *Eur J Hum Genet* 8:480–486.
99. Villemans R, Homo sapiens *Mitochondrial DNA D-Loop HVRI Sequence*. Available at <http://www.ncbi.nlm.nih.gov/nuccore>; accession numbers AJ274757–AJ274942.
100. Irwin J, et al. (2008) Mitochondrial control region sequences from northern Greece and Greek Cypriots. *Int J Legal Med* 122:87–89.
101. Kovatsi L, Saunier JL, Irwin JA (2009) Population genetics of Y-chromosome STRs in a population of Northern Greeks. *Forensic Sci Int Genet* 4:e21–e22.