

Early Modern Eurasians

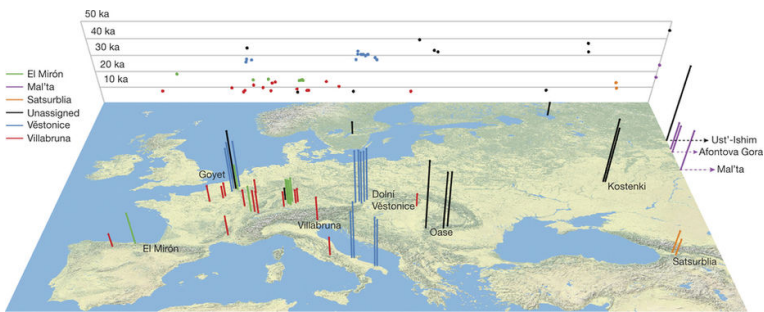
Alan R. Rogers

October 19, 2021

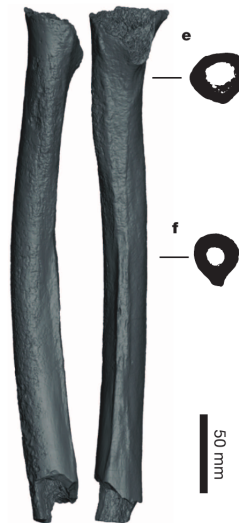
Outline

- ▶ Paleolithic Eurasia
- ▶ Mesolithic Eurasia

Paleolithic DNA of NW Eurasia



Note time scale at back.

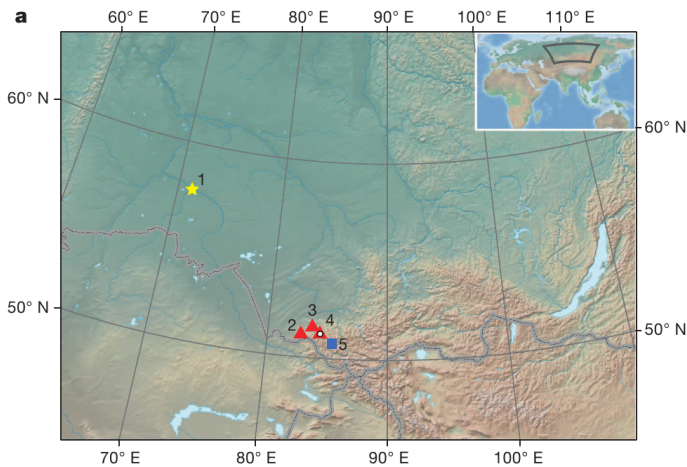


Ust'-Ishim: a 45-ky-old modern man from W Siberia

Excavated 2008

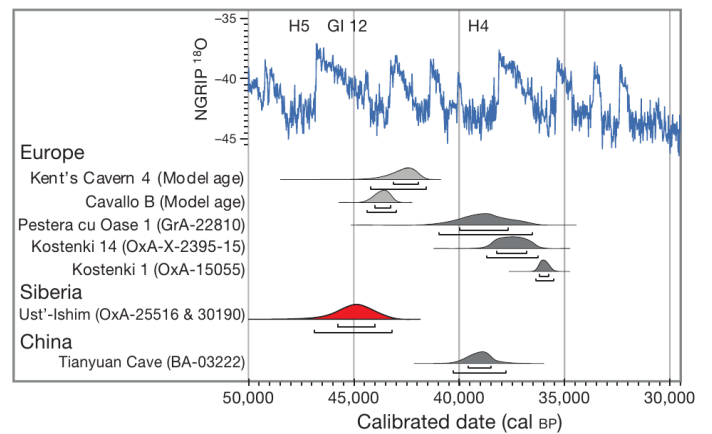
Fu et al. (2014)

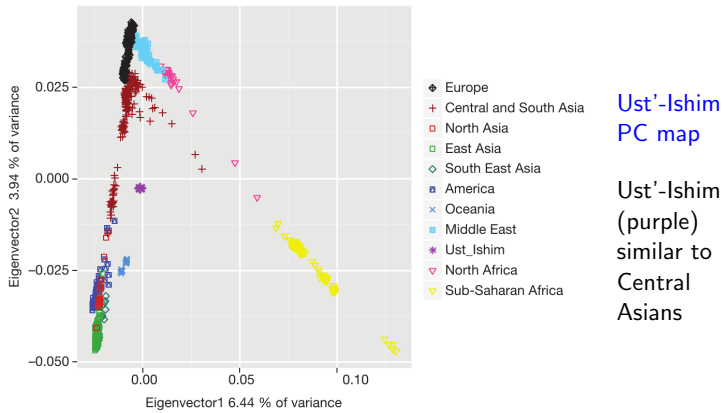
Location of Ust'-Ishim



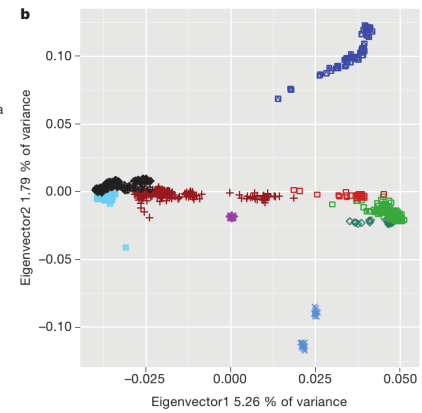
1, Ust'-Ishim; 4, Denisova.

Dates and temperature



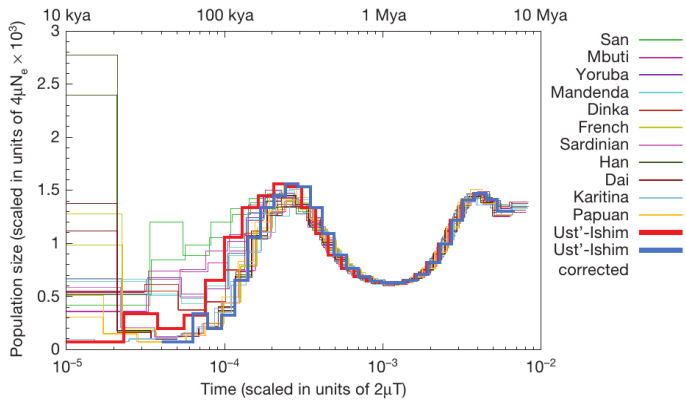


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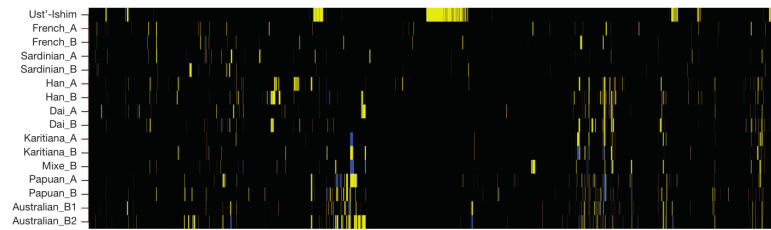
History of population size



Red, assumes Ust'-Ishim lived today; Blue, fits curve to others and estimates mutation rate. Lived during late Pleistocene bottleneck.

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Neanderthal allele sharing



Ust'-Ishim has 2.3% Neanderthal DNA—in big chunks. Implies recent admixture (50–60 kya).

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Conventional wisdom

- ▶ Early emigration out of Africa to Australia & New Guinea.
- ▶ Later northern emigration.
- ▶ Ust'-Ishim should be part of northern population.

Problem

Ust'-Ishim is equally related to northern and southern modern populations. Did its population go extinct?

I doubt it: Ust'-Ishim is similar to modern Central Asians.

Oase 1



Man from Peștera cu Oase, Romania

40 ky-old

6–9% of genome is Neanderthal—3× larger than any other

3 Neanderthal segments >50 cM

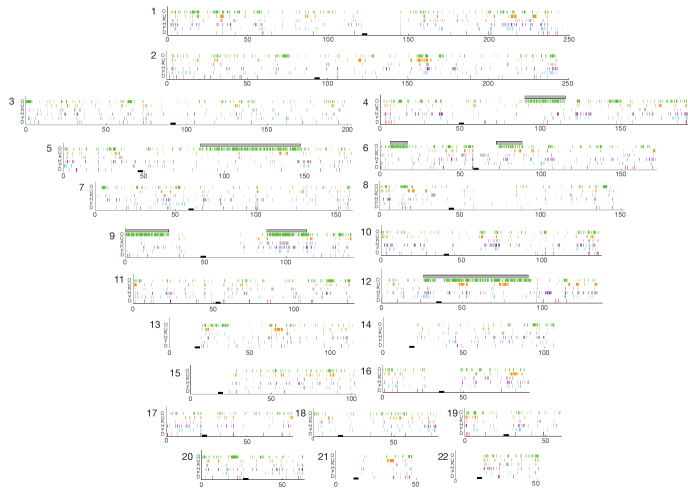
Implies Neanderthal ancestor 4–6 generations back.

Shares more derived alleles with E Asians & Native Americans than with Europeans.

Fu et al. (2015)

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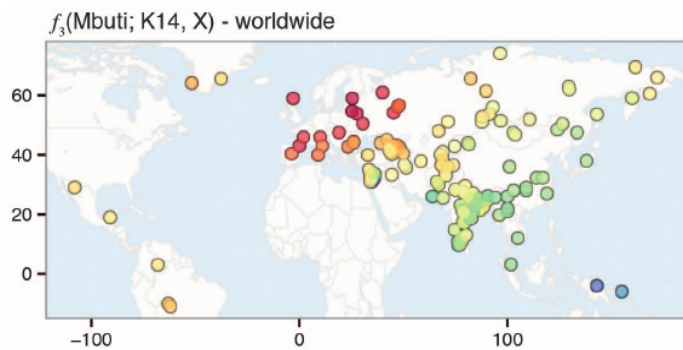


Green: Oase1 alleles shared with Neanderthal.

Kostenki 14: a 37 ky old Russian man



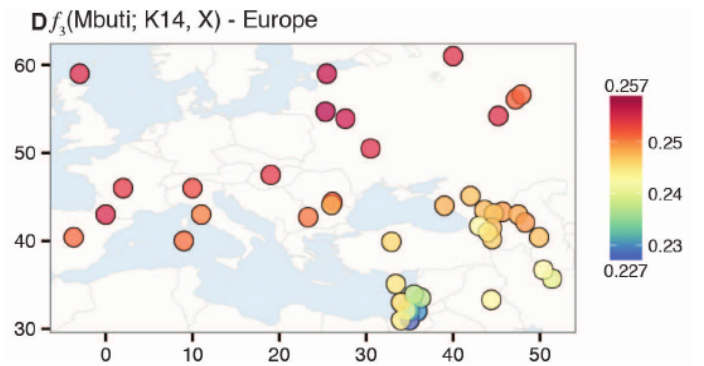
Affinities of Kostenki with world populations



(Seguin-Orlando et al. 2014)

Similar to Northern Europeans.

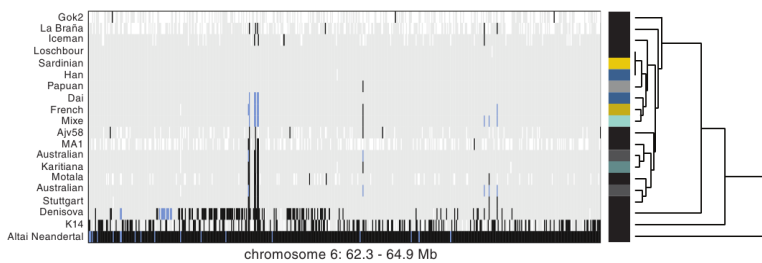
Affinities of Kostenki with European populations



(Seguin-Orlando et al. 2014)

Similar to northern and western Europeans.

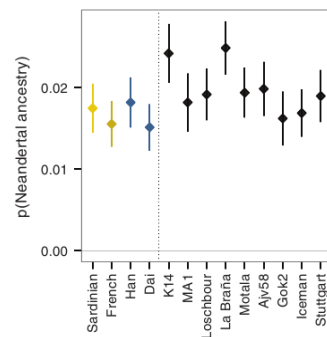
Neandertal allele sharing



(Seguin-Orlando et al. 2014)

K14 has more Neandertal DNA and in bigger chunks.

Neandertal admixture fraction



(Seguin-Orlando et al. 2014)

Kostenki (K14) had more Neandertal DNA than modern humans and in bigger chunks. Implies recent admixture—54 kya.

24 ky old burial from Mal'ta, Siberia



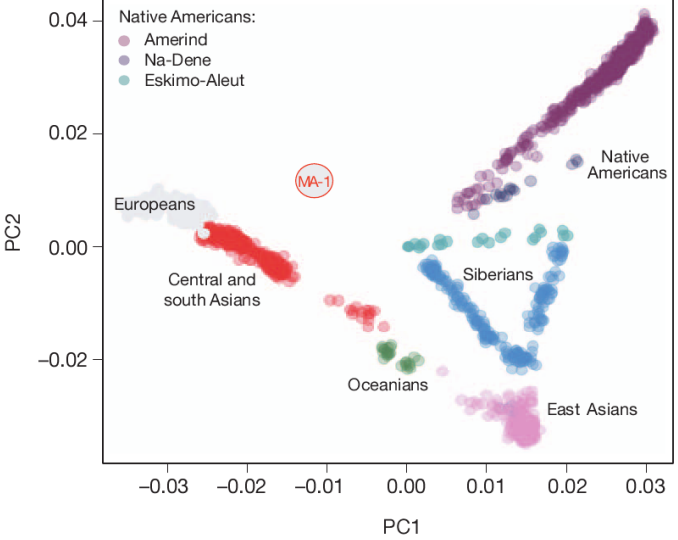
(Raghavan et al. 2013)

Location of Mal'ta site

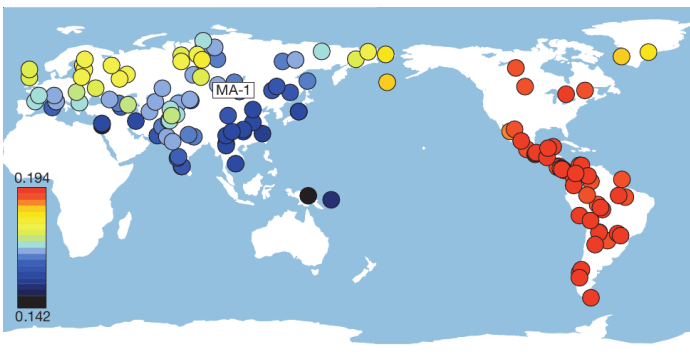


Raghavan et al. (2013)

Mal'ta in principal components map



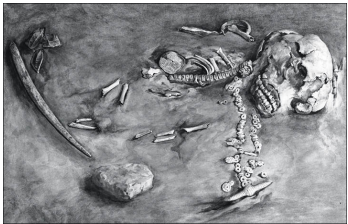
Affinities of Mal'ta with other populations



(Raghavan et al. 2013)

Similar to Amerindians and Northern Europeans.

24 ky old burial from Mal'ta, Siberia



(Raghavan et al. 2013)

- ▶ 1/3 of ancestry shared with Native Americans and Europeans
- ▶ European mitochondrial DNA

mtDNA haplogroups: 45–25 kya



(Posth et al 2016)

mtDNA haplogroups: 19.5–14.5 kya



(Posth et al 2016)

mtDNA haplogroups: 14.5–11.5 kya

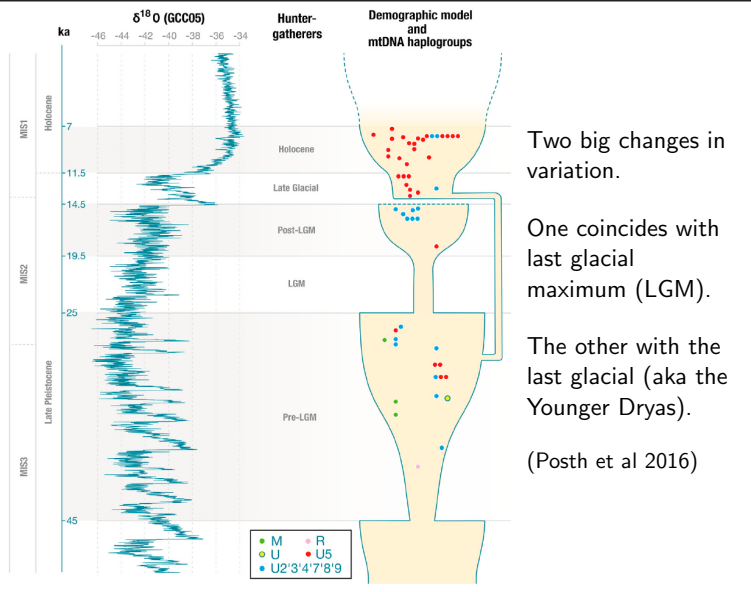


(Posth et al 2016)

mtDNA haplogroups: 11.5–7 kya



(Posth et al 2016)



Outline

- Archaeology and paleontology
- Expansion out of Africa
- Paleolithic Eurasia
- ▶ Mesolithic Eurasia

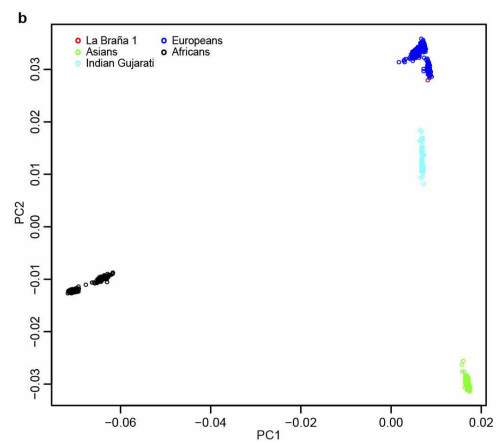
La Braña: a 7,000 y old forager



La Braña site

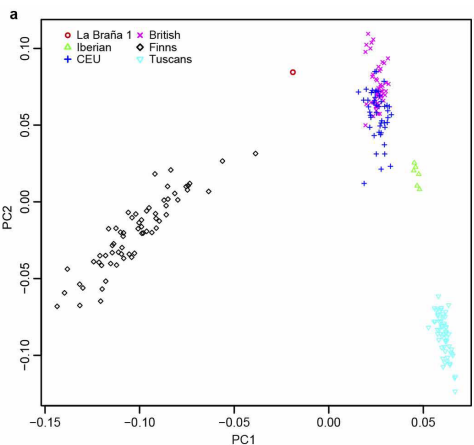


La Braña PC Map: World



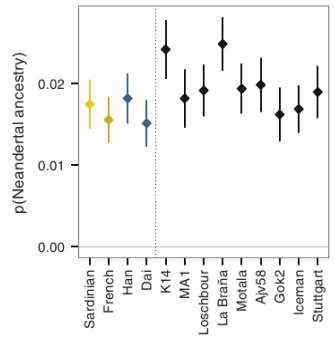
On world-wide scale, La Braña is European.

La Braña PC Map: Europe



But La Braña is not like modern Europeans.

Neandertal admixture fraction



La Braña had more Neandertal DNA than modern humans.

(Seguin-Orlando et al. 2014)

La Braña adaptations

- ▶ Dark skin
 - ▶ Blue eyes
 - ▶ Lactose intolerant
 - ▶ Poor at digesting starch.
 - ▶ Modern allele at 24 of 40 loci affecting immune function.
- These observations suggest that the Neolithic transition did not drive all cases of adaptive innovation on immunity genes found in modern Europeans.*
- (Olalde et al 2014)

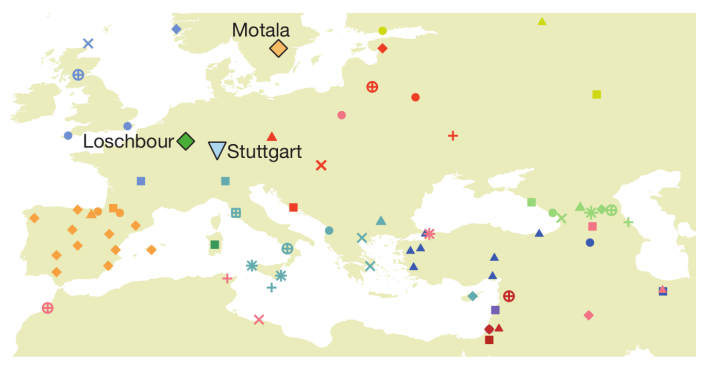
Study of Lazaridis et al (2014)

DNA sequences of:

Label	Location	Samples	Age	Description
Loschbour	Luxembourg	1	8 ky	forager
Motala	Sweden	7	8 ky	forager
Stuttgart	Germany	1	7 ky	farmer
	Europe	2345	0 ky	modern

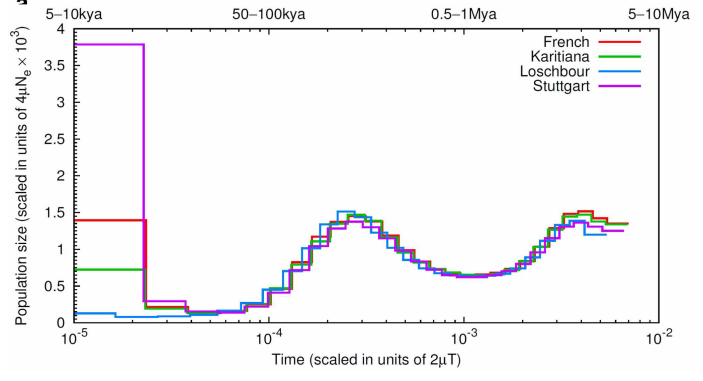
The moderns were not sequenced but were genotyped at 594,924 autosomal single-nucleotide polymorphisms.

Lazaridis et al samples



Loschbour, Motala: 8 ky old foragers; Stuttgart: 7 ky old farmer.

Population size

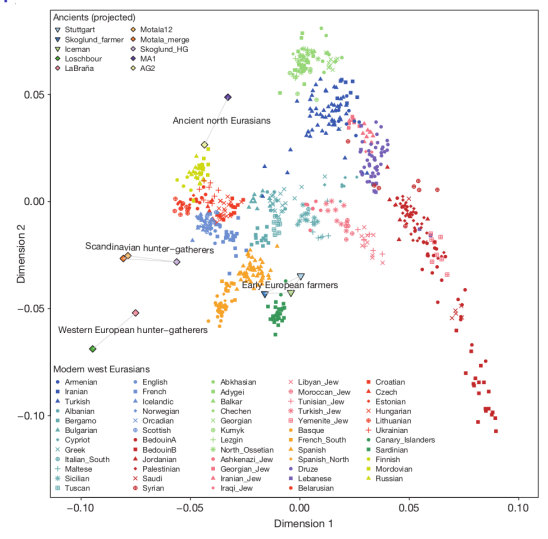


Loschbour: 8 ky old forager; Stuttgart: 8 kya farmer; others: modern. **No post-Pleistocene growth of forager population.**

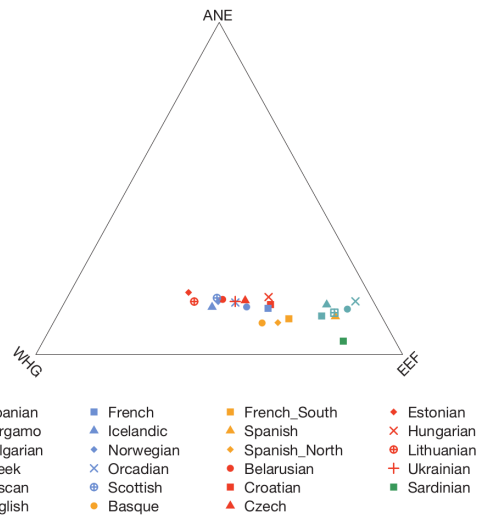
Contributions to modern Europeans

- ANE Ancient North Eurasian
- WHG West-European hunter-gatherer
- EEF Early European Farmer

PCA map



Contributions to modern Europeans



Adaptations

- ▶ Lochbour (forager) relatively good at digesting starch, even before agriculture.
- ▶ Stuttgart (farmer): Dark hair, light skin, brown eyes.
- ▶ Foragers: Dark skin, hair and blue eyes.
- ▶ But one Motala (forager) sample had one copy of light skin allele. It was in Europe before agriculture.

Summary

- ▶ Genome of Ust'-Ishim, a 45-ky-old Siberian, was modern, distinct from Africans, similar to Central Asians. Big chunks of Neanderthal genome imply recent admixture.
- ▶ Kostenki, a 36 ky-old Siberian, genetically similar to Europeans. More Neanderthal DNA than modern humans.
- ▶ Mal'ta, 24-ky-old Siberian, shared ancestry with Native Americans and Europeans.
- ▶ European mitochondrial haplogroups were diverse at first. Lost diversity during last glacial maximum (20 kya) and the Younger Dryas (12 kya). Regained it during Holocene (after 11 kya).
- ▶ La Braña, a 7-ky-old forager from Spain. More similar to modern Europeans than to Asians or Africans, but not like any modern European. See slides on adaptations.