

Gli antenati delle razze bovine:
DNA antico e moderno per ricostruire l'evoluzione e la
domesticazione dell'uro

Giorgio Bertorelle



Bos primigenius

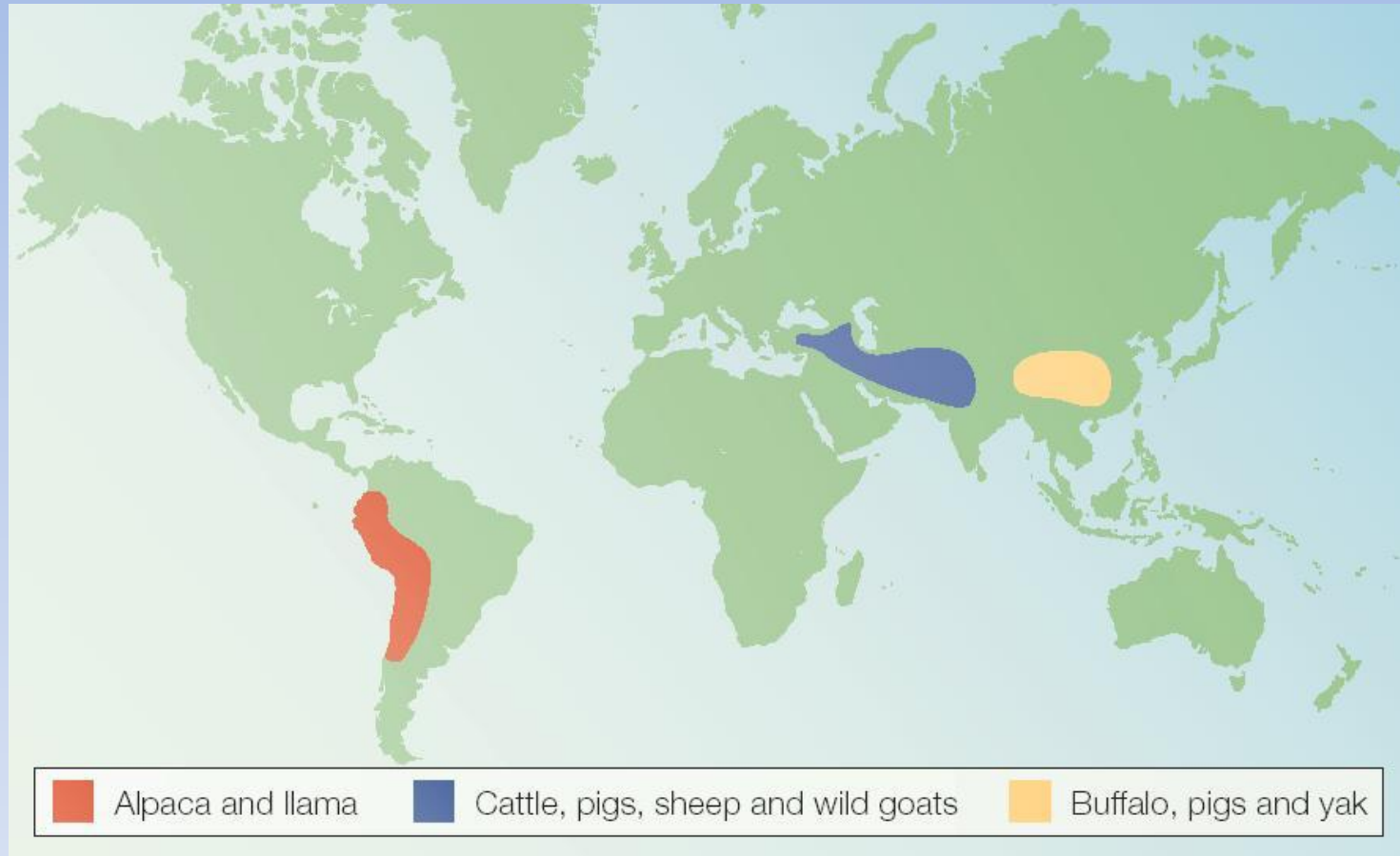


Bos taurus

Some reasons to study the domestication events

1. Understanding the pattern and the consequences of strong (and rapid) selective regimes
2. Understanding the effects on wild species (for example, hybridization between wild and domestic forms)
3. Understanding (how, where, when, why) a fundamental step in our history
4. Understanding the genetic consequences on humans
5. Reconstructing human migrations

Major domestication areas



Bruford et al, 2003

Modern DNA and domestication

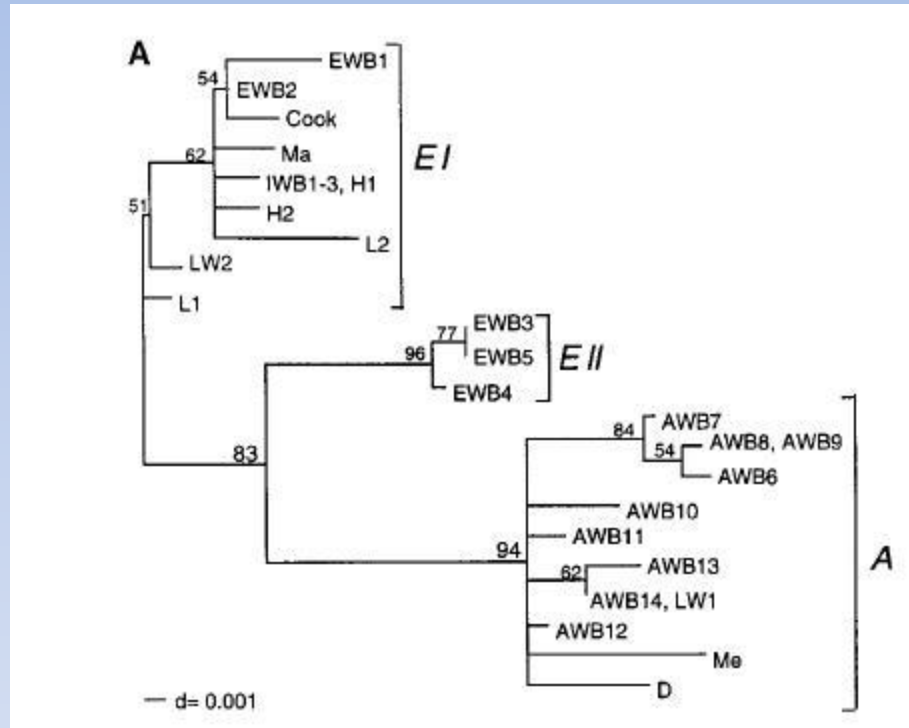
Evidence mainly based on mtDNA sequences (structure and phylogeography of the tree) in wild (if available) and domestic forms.

Classical inferences from genetic data:

if the tree is phylogeographically structured in X clades, and the divergence of the clades is very ancient, at least X domestication events occurred.

The pig

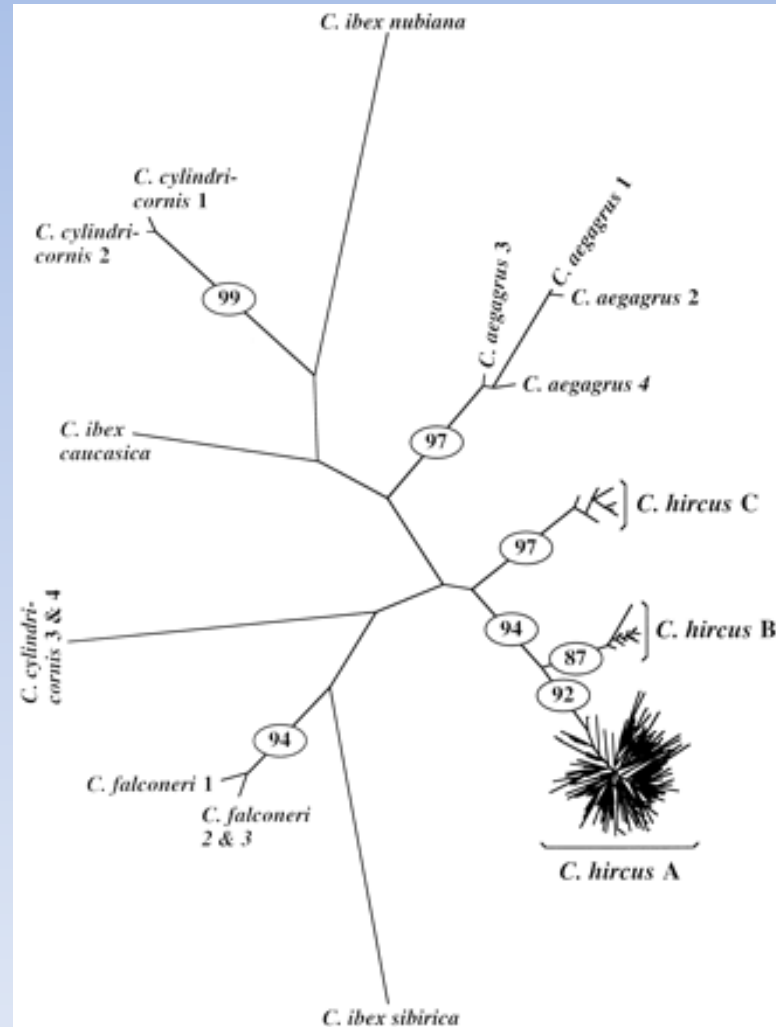
(2 events, from 2 wildboar groups)



Giuffra et al, 2000

The goat

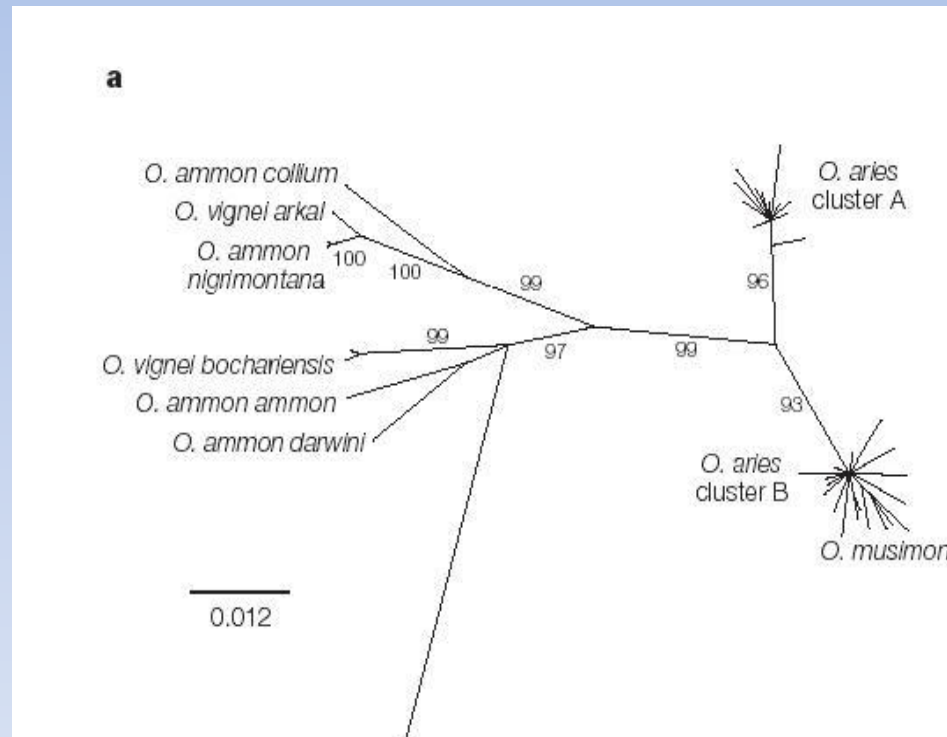
(3 events, from 3 wild goat groups)



Luikart et al, 2001

The sheep

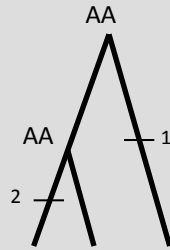
(2 events, from 2 mouflon groups)



Hiendleder et al, 2002

Networks to represent recent genealogies

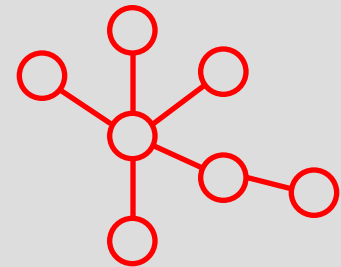
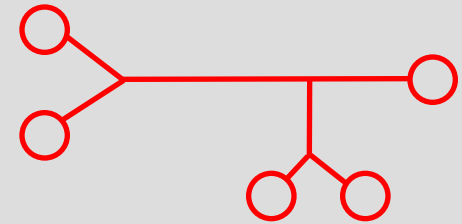
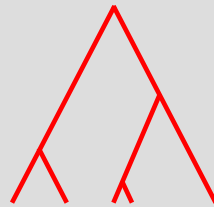
From genealogies...



... to networks

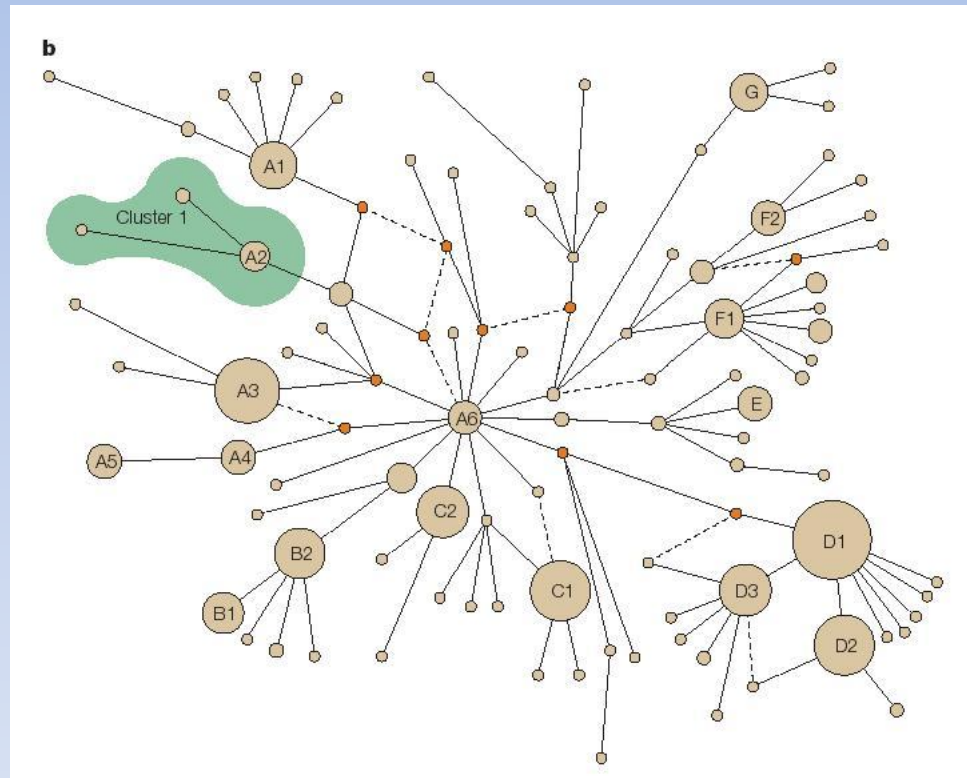


Different genealogy shapes correspond to different network shapes



The horse

Complex tree (no clear structure):
multiple domestication?



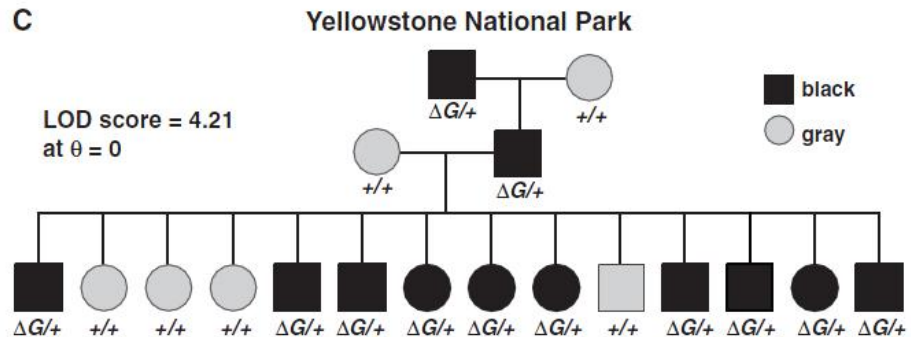
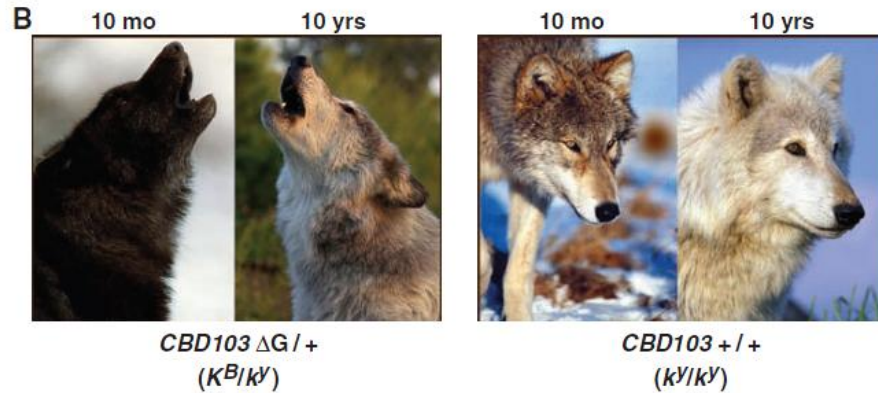
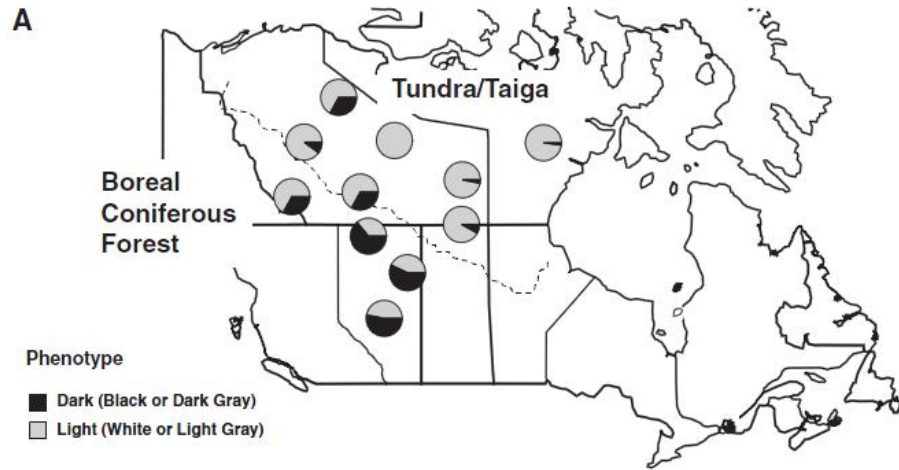
Jansen et al, 2002

Molecular and Evolutionary History of Melanism in North American Gray Wolves

Tovi M. Anderson,¹ Bridgett M. vonHoldt,² Sophie I. Candille,¹ Marco Musiani,³ Claudia Greco,⁴ Daniel R. Stahler,^{2,5} Douglas W. Smith,⁵ Badri Padhukasahasram,⁶ Ettore Randi,⁴ Jennifer A. Leonard,⁷ Carlos D. Bustamante,⁶ Elaine A. Ostrander,⁸ Hua Tang,¹ Robert K. Wayne,² Gregory S. Barsh^{1*}

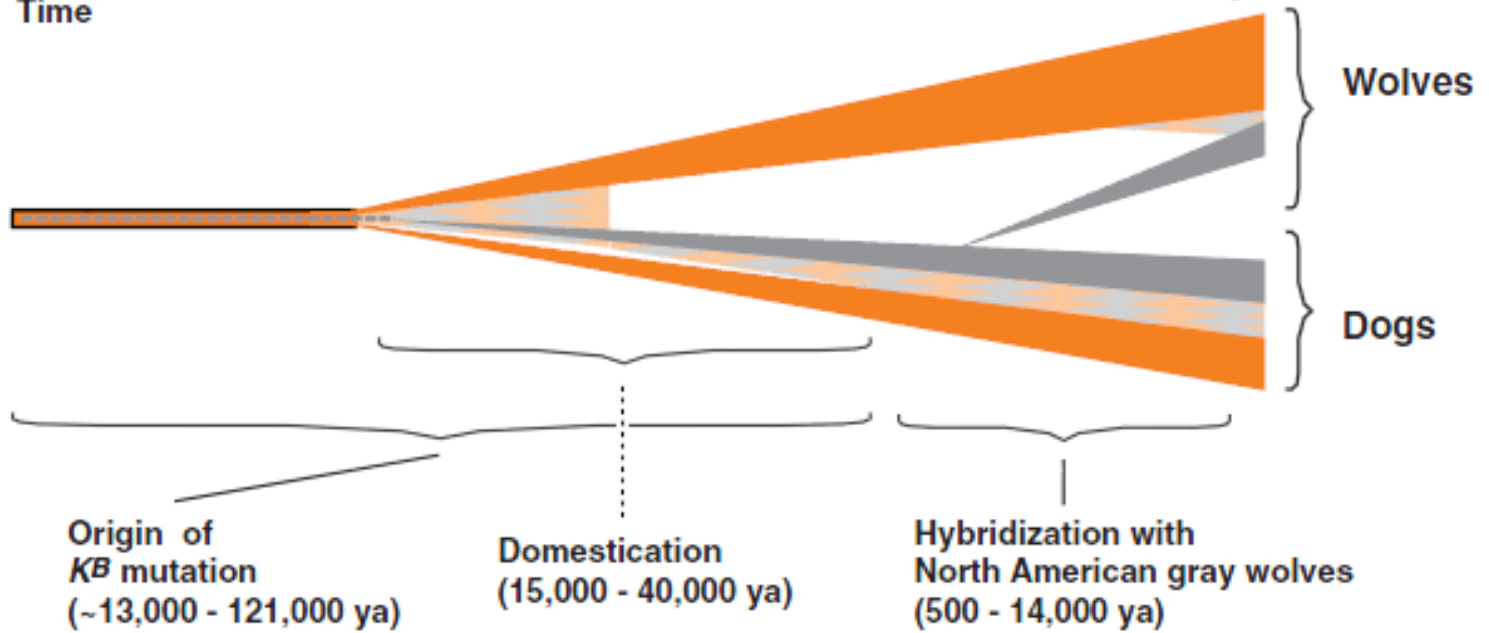
Morphological diversity within closely related species is an essential aspect of evolution and adaptation. Mutations in the *Melanocortin 1 receptor (Mc1r)* gene contribute to pigmentary diversity in natural populations of fish, birds, and many mammals. However, melanism in the gray wolf, *Canis lupus*, is caused by a different melanocortin pathway component, the *K* locus, that encodes a beta-defensin protein that acts as an alternative ligand for Mc1r. We show that the melanistic *K* locus mutation in North American wolves derives from past hybridization with domestic dogs, has risen to high frequency in forested habitats, and exhibits a molecular signature of positive selection. The same mutation also causes melanism in the coyote, *Canis latrans*, and in Italian gray wolves, and hence our results demonstrate how traits selected in domesticated species can influence the morphological diversity of their wild relatives.

Fig. 1. Distribution of melanism and *K* locus genotypes in North American gray wolves. (A) Location and coat color phenotype of Canadian samples used here and as described (4). (B) Age-related graying and the associated difficulty of inferring genotype from phenotype in gray animals. Each pair of photos shows the same individual at different ages (10 months and 10 years) and documents an increasingly gray appearance at 10 years, reflecting the dilution of eumelanin in the K^B/k^Y individual (left pair of images) and dilution of both eumelanin and pheomelanin in the k^Y/k^Y individual (right pair of images). [Images courtesy of Monty Sloan, Wolf Park, Battle Ground, Indiana] (C) Co-segregation of K^B and black coat color in a three-generation pedigree from the Leopold pack in Yellowstone National Park (17). ΔG indicates the dominant K^B allele, whereas + indicates the wild-type allele, k^Y .



D

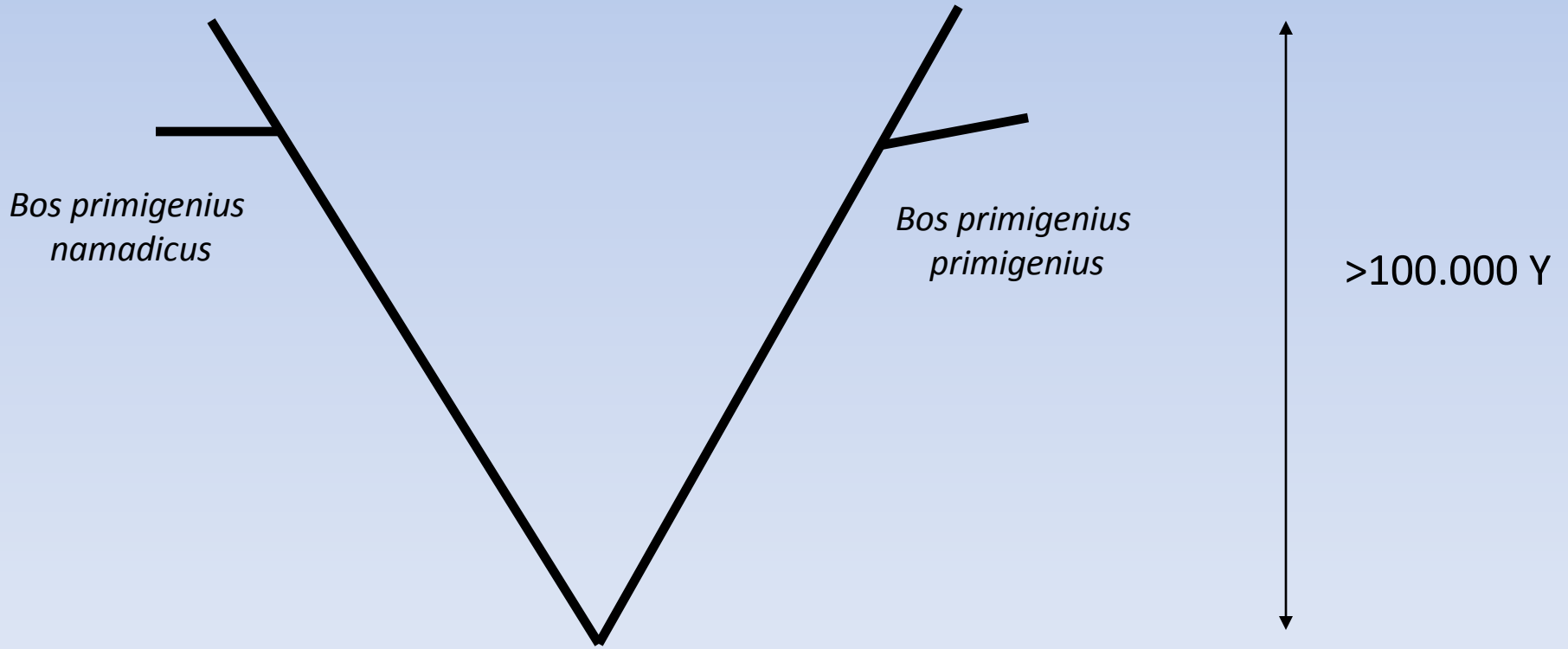
Time

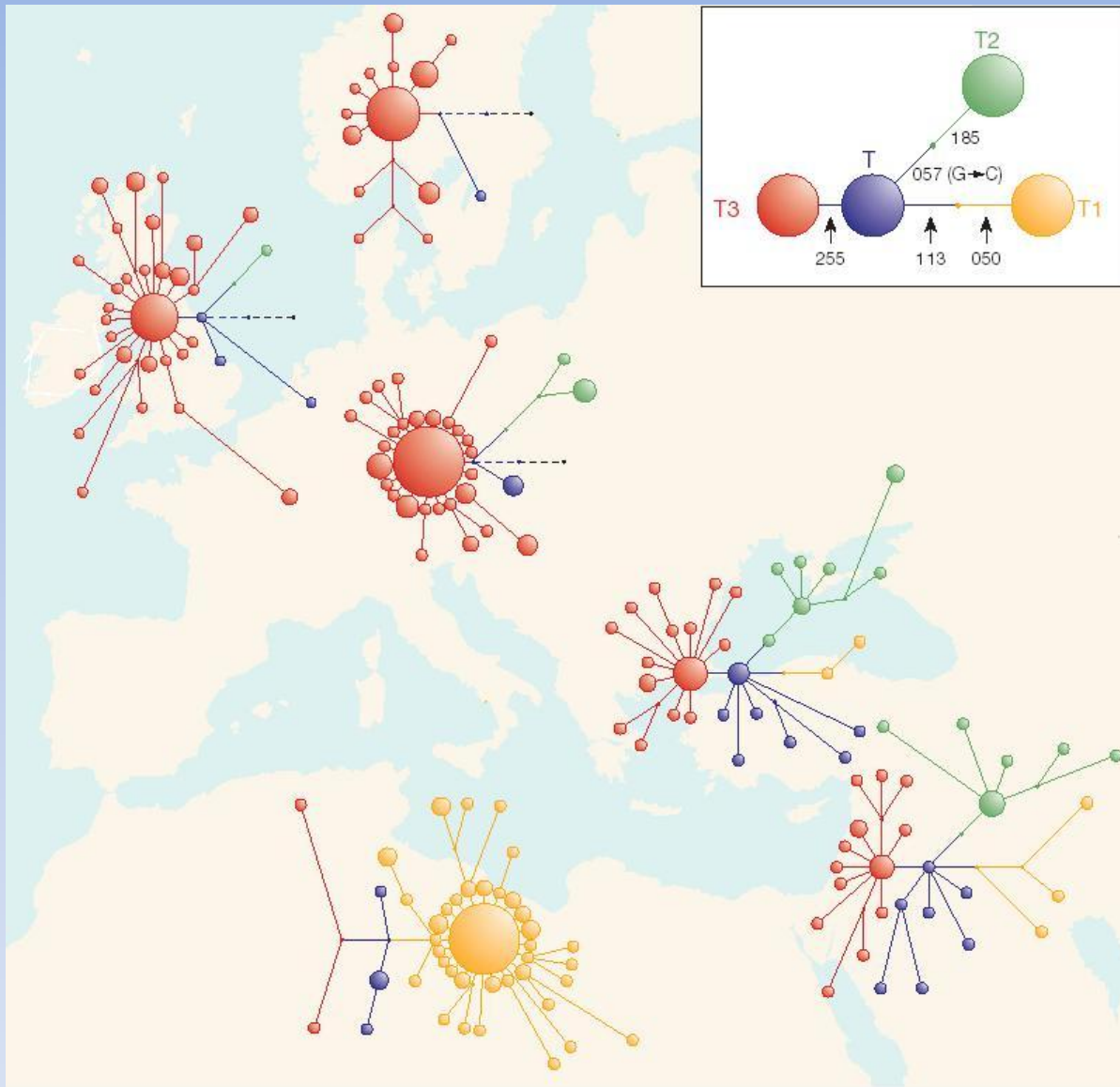


Bos indicus



Bos taurus

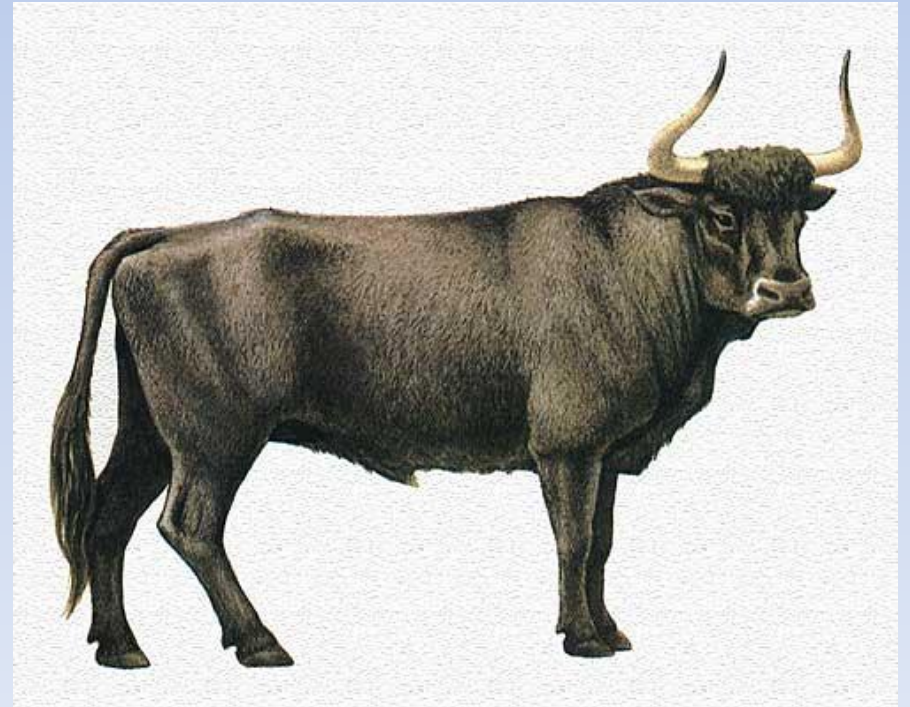






Who was the cattle ancestor?

What about its DNA?







Bos primigenius heck...

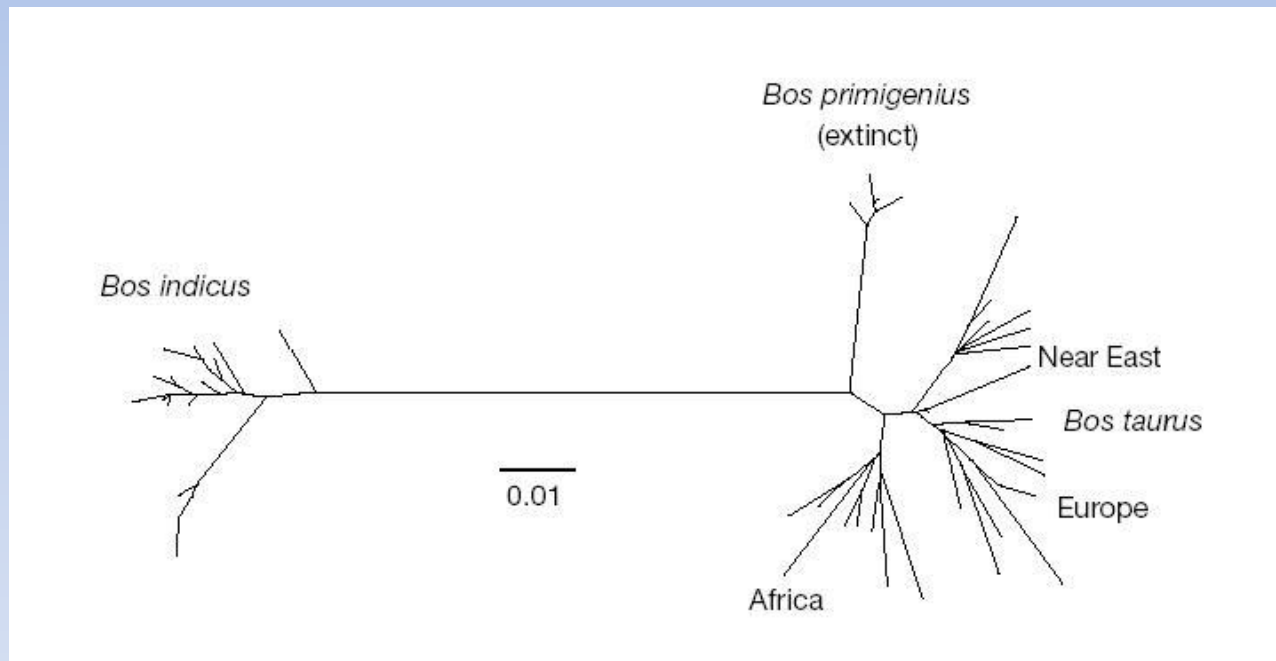


Podolica



Devon

The DNA from British aurochs seems to confirm the single origin, excluding the genetic contribution of European aurochs into European cattle



Bayley et al, 1996

Molecular marker of domestication...

mtDNA analysis of 5 Southern Italian aurochs

1. Bosp8 17,100±300 (Grotta Paglicci, Fg)
2. Bosp9 16,260±160 (Grotta Paglicci, Fg)
3. Bosp82 15.860±80 (Grotta delle Mura, Ba)
4. BospB between 11,420±100 BP and 15,860±80 (Grotta delle Mura, Ba)
5. BospS about 7,000 (Termini Imerese, Pa)

The origin of European cattle: Evidence from modern and ancient DNA

Albano Beja-Pereira^{a,b,c}, David Caramelli^{c,d}, Carles Lalueza-Fox^e, Cristiano Vernesi^f, Nuno Ferrand^{a,g}, Antonella Casoli^h, Felix Goyacheⁱ, Luis J. Royoⁱ, Serena Conti^{d,j}, Martina Lari^g, Andrea Martini^g, Lahousine Ouragh^k, Ayed Magid^l, Abdulkarim Atash^l, Attila Zsolnai^m, Paolo Boscatoⁿ, Costas Triantaphylidis^o, Konstantoula Ploumi^p, Luca Sineo^q, Francesco Mallegni^r, Pierre Taberlet^h, Georg Erhardt^t, Lourdes Sampietro^s, Jaume Bertranpetit^t, Guido Barbujani^u, Gordon Luikart^{b,c}, and Giorgio Bertorelle^{s,u,v}

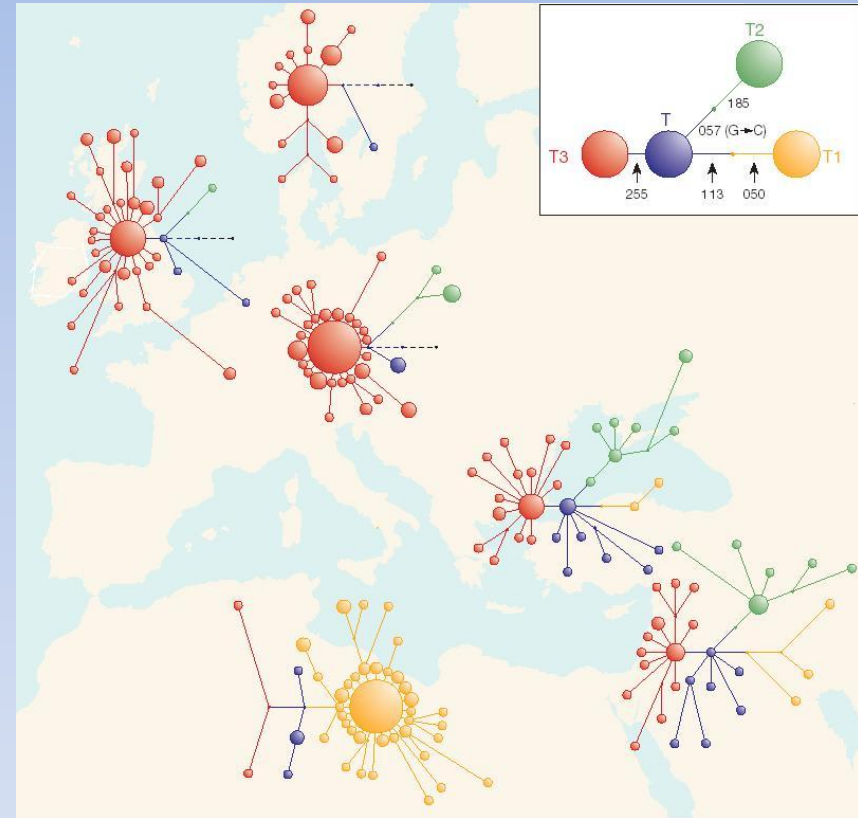


11111111111111111111111111
 66666666666666666666666666
 0000000000111112222233
 445555578901248356800
 290157845393215154412
 TCCTTGCTTGTGTTGCTCGCG

T3
 T1 ..T.....C....C....
 T2C.....A.C....
 T4 C.....A.....A

Bos8
 BosB??????
 BosS??????
 Bos9 C.....A..
 Bos82 ..T.....C.....????

BR-A1 .T.C..TCC...C.?TCA...
 BR-A2 .T.CC.TCC...C.?TCA...
 BR-A3 .T.C..TCC...CC.TCA...
 BR-A4 .T.C..TCC.C.C..TCA.C..
 BR-A5 .TTC..TCC...C..TCA...
 BR-A6 .T.C..TCC...C..TCA...



New DNA data from ancient specimens

- 12 additional aurochs in Italy (from 56 initially available)
- Complete mtDNA genome from one individuals
- More data (55 sequences) in other European regions

Lari et al. *BMC Evolutionary Biology* 2011, **11**:32
<http://www.biomedcentral.com/1471-2148/11/32>

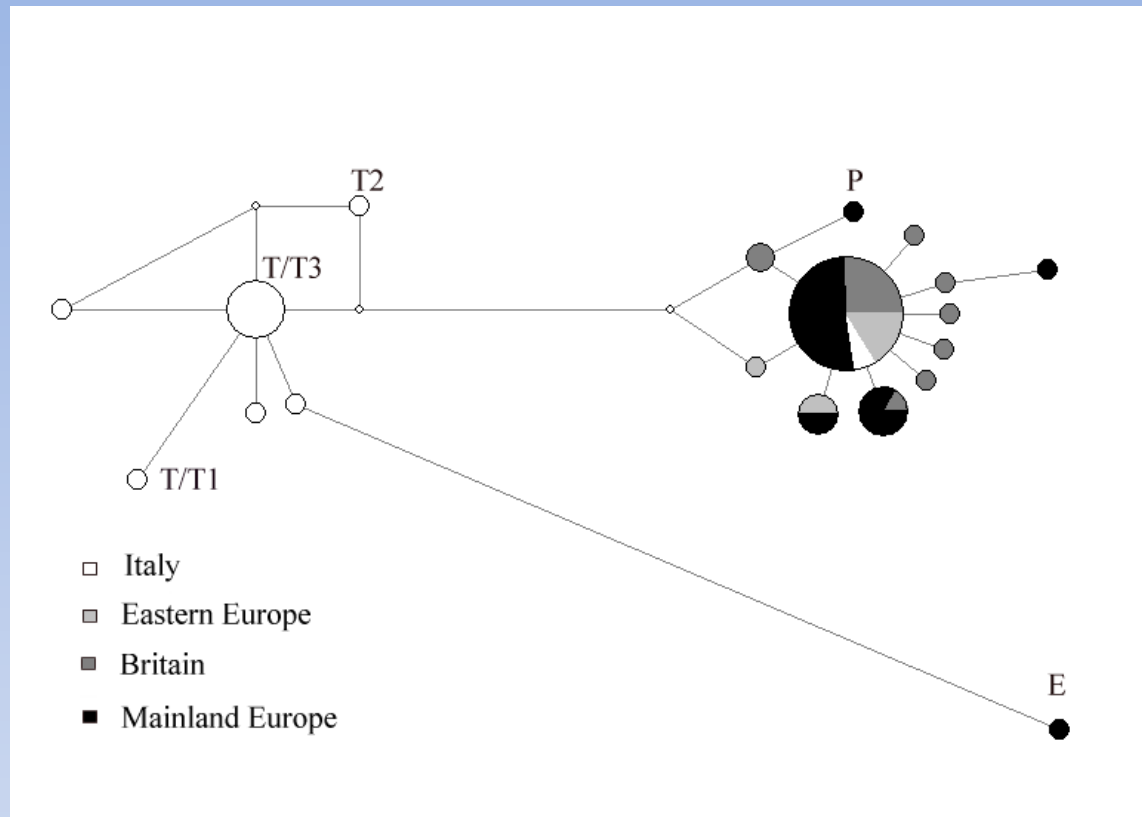


RESEARCH ARTICLE

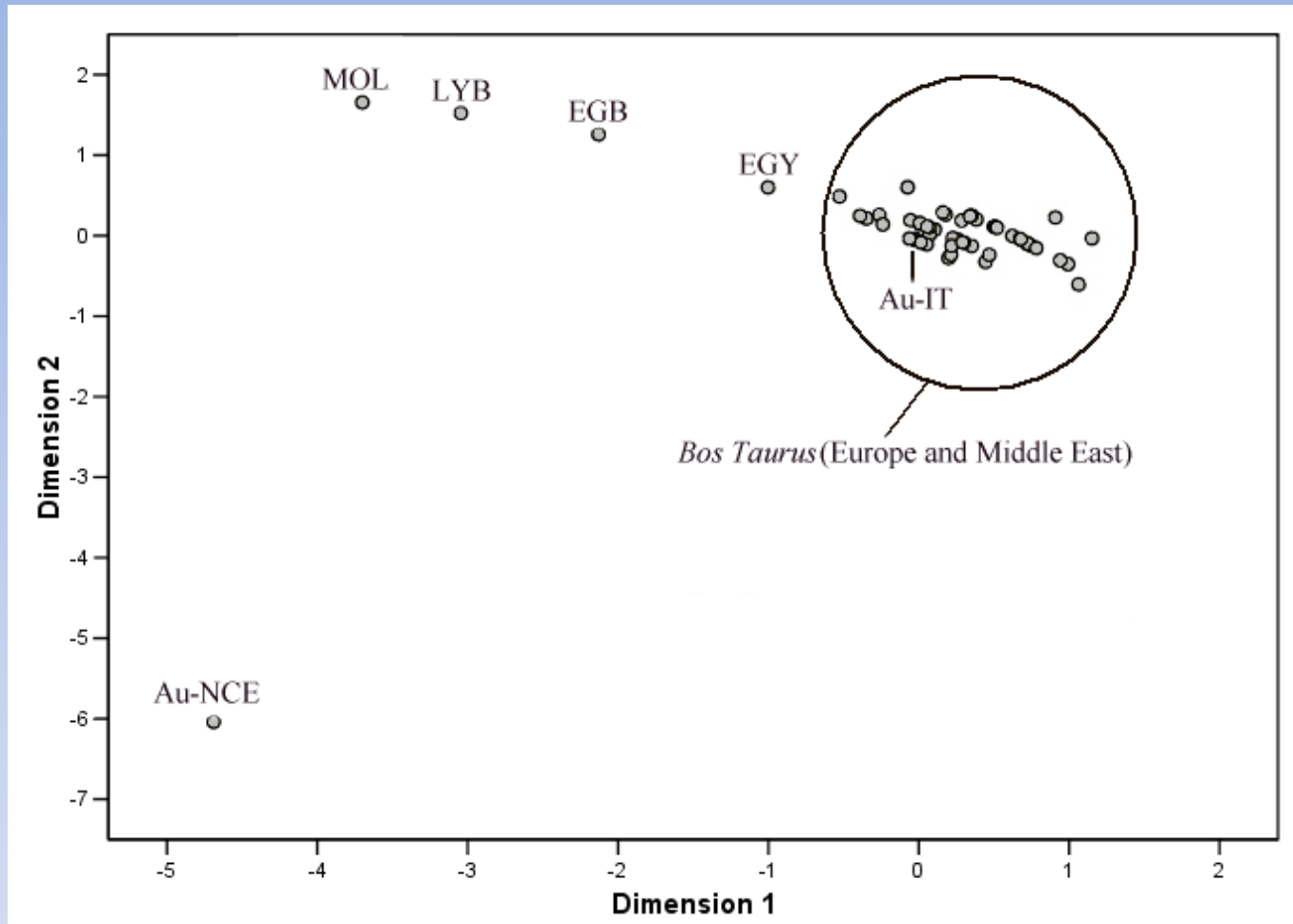
Open Access

The Complete Mitochondrial Genome of an 11,450-year-old Aurochs (*Bos primigenius*) from Central Italy

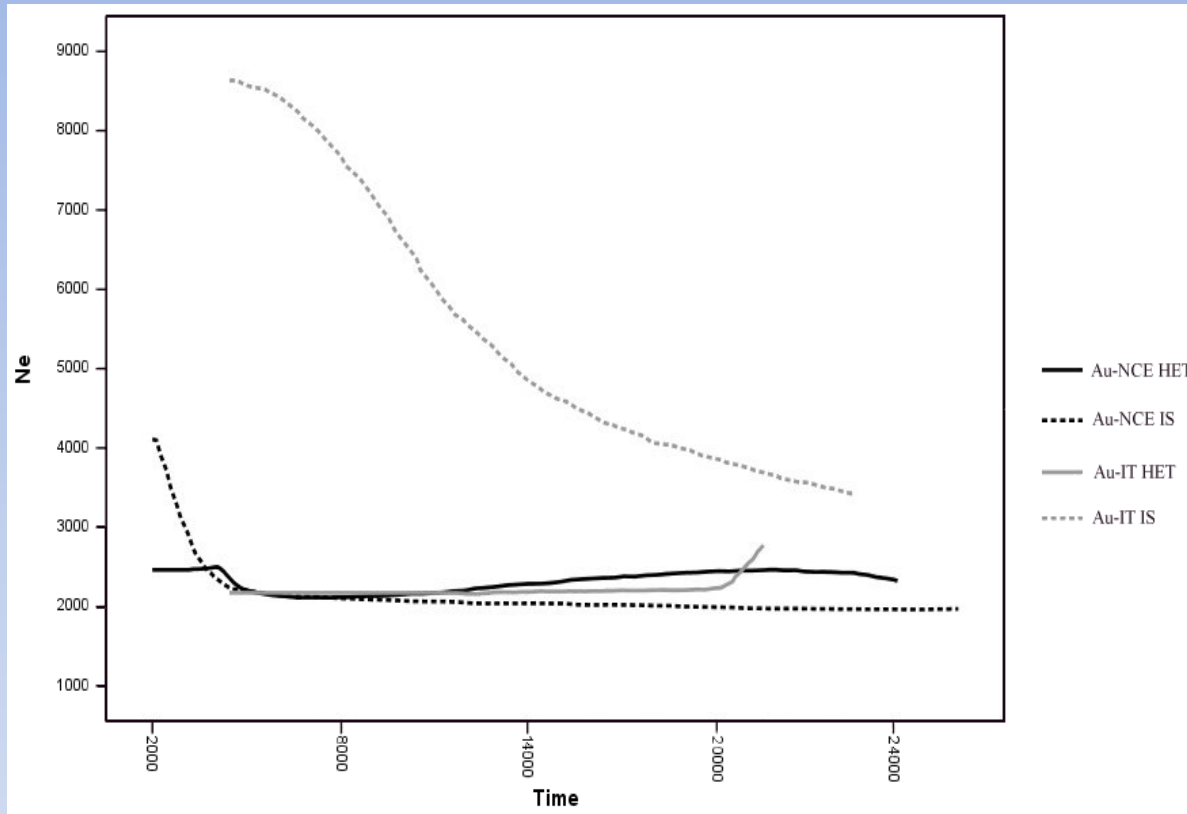
Martina Lari¹, Ermanno Rizzi², Stefano Mona^{3,8}, Giorgio Corti², Giulio Catalano¹, Kefei Chen⁴, Cristiano Vernesi⁵, Greger Larson⁶, Paolo Boscato⁷, Gianluca De Bellis², Alan Cooper⁴, David Caramelli¹, Giorgio Bertorelle^{3*}



- In Italy, we confirm that the most frequent aurochs mtDNA sequences belong to the T “cattle” type (but we observe also 2 typical Northern European haplotypes)
- Complete mtDNA genome is T type, with some substitutions
- In Central-Northern Europe, sequences only of the P type



Italian aurochs cluster with European cattle breeds



Italian and European aurochs probably did not expand demographically