# The spread of the Neolithic in Europe: simulations versus archaeological and genetic data

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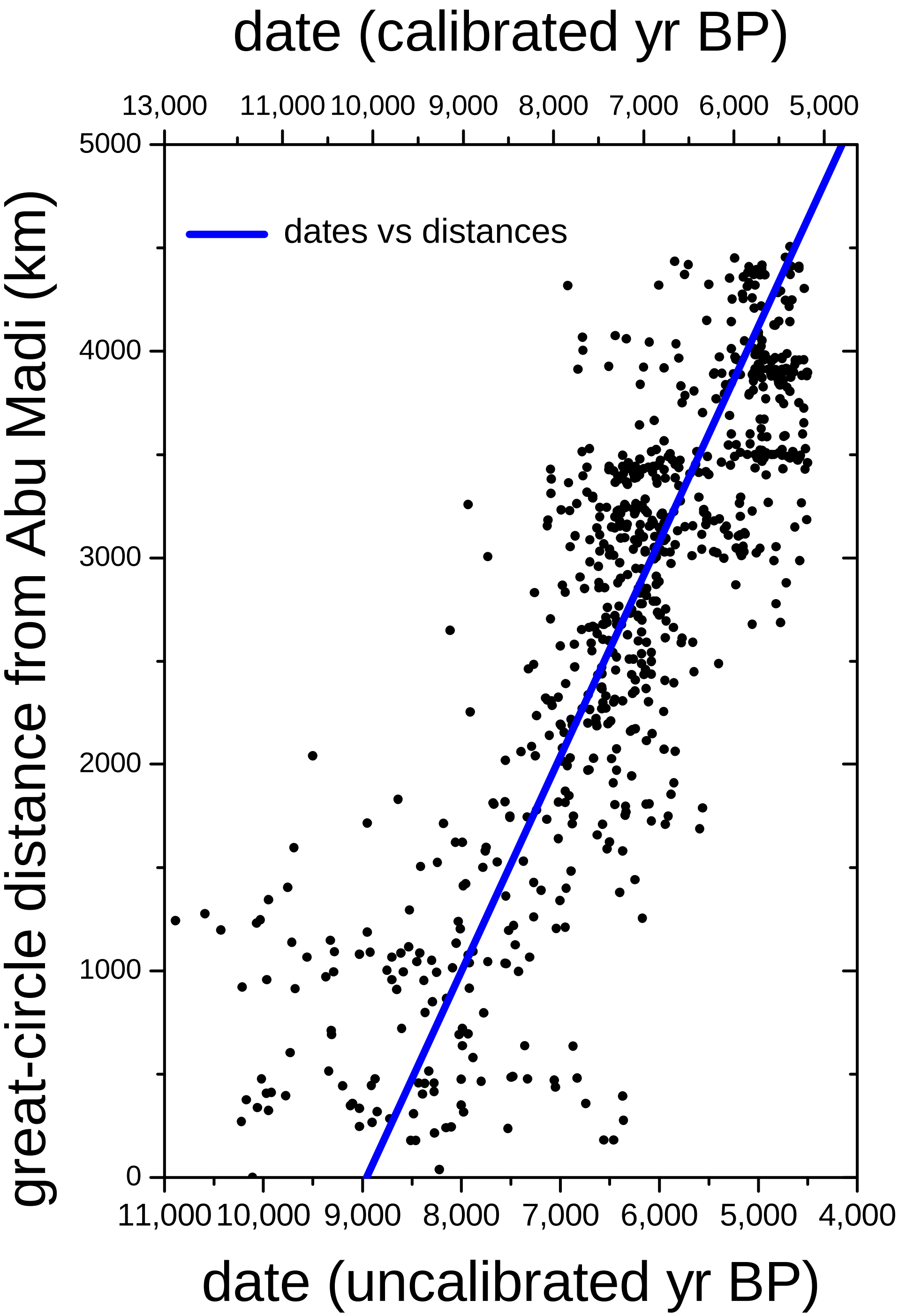
Dedicated to the memory of Luca Cavalli-Sforza

# Models of Neolithic transitions

- **Demic diffusion** = spread of farming populations = dispersal + net reproduction

- **Cultural diffusion** = spread of ideas = transmission of plants, animals and knowledge from farmers to hunter-gatherers (acculturation).

- **Demic-cultural models**




# What is the observed spread rate?

# 0.9-1.3 km/yr

735 sites in Europe & Near East

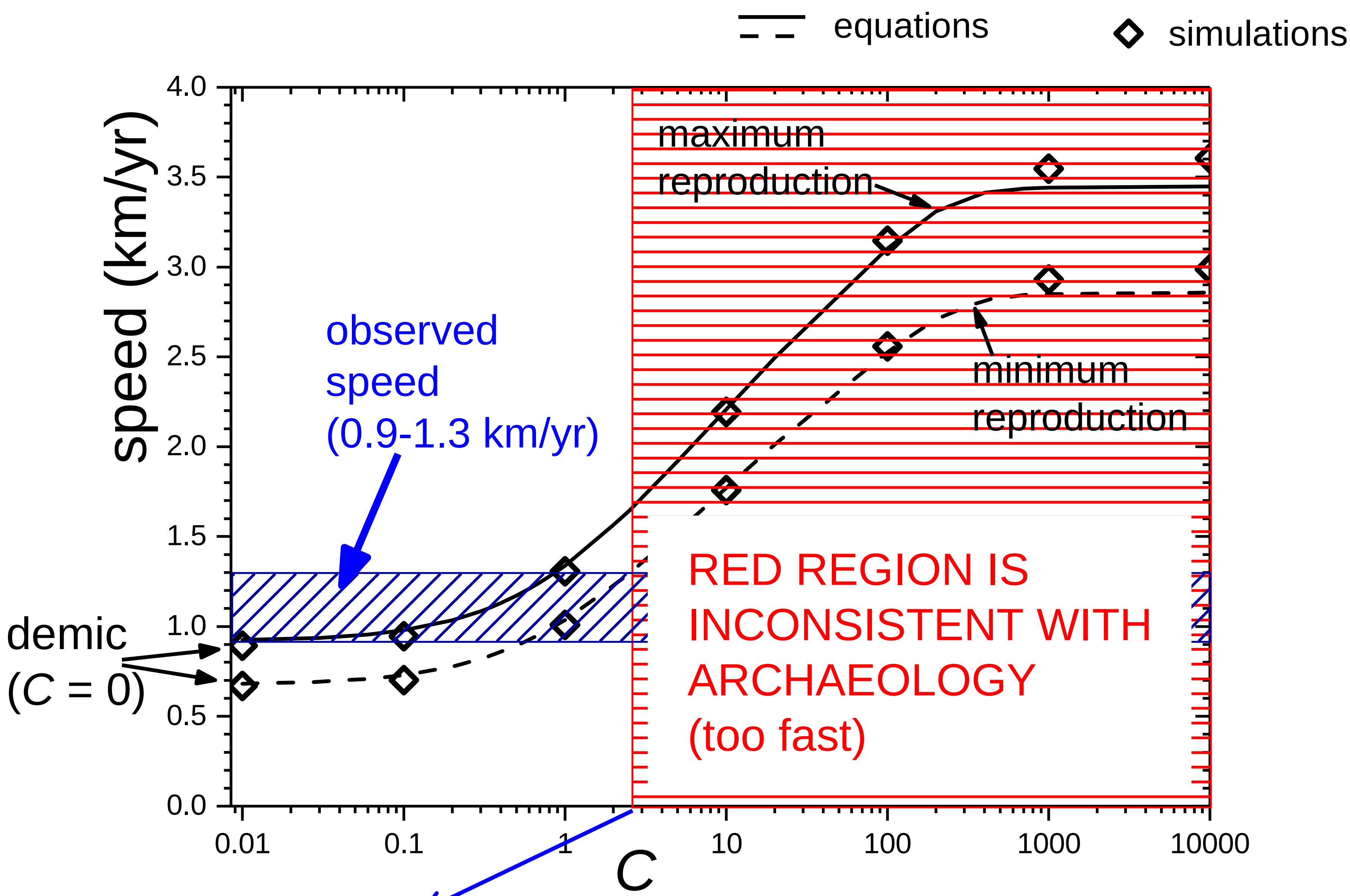
$r = 0.83$

highest-*r* origins

great circles & shortest paths

slopes of dates vs distances

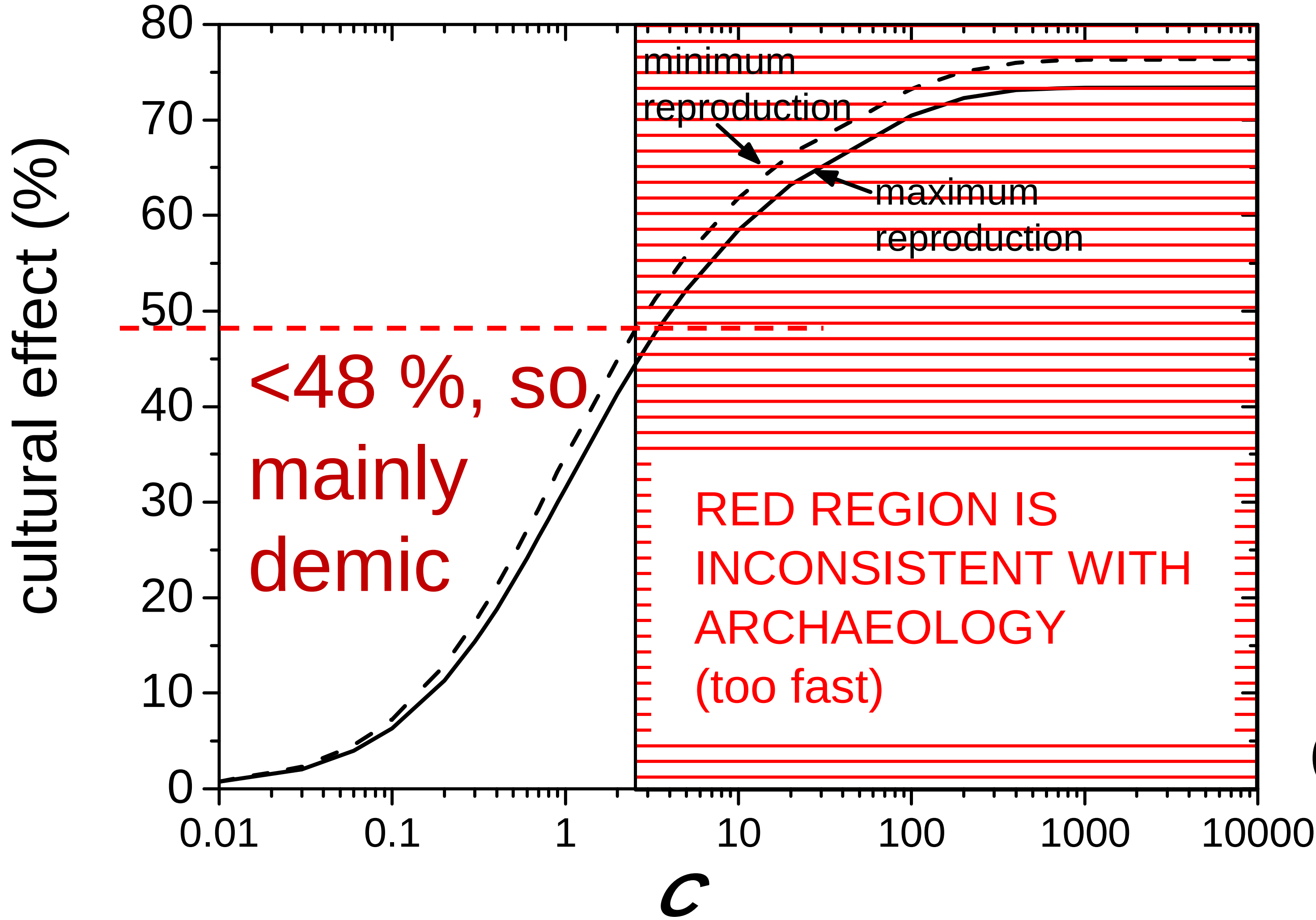
Pinhasi, Fort & Ammerman, *PLoS Biol.* (2005)



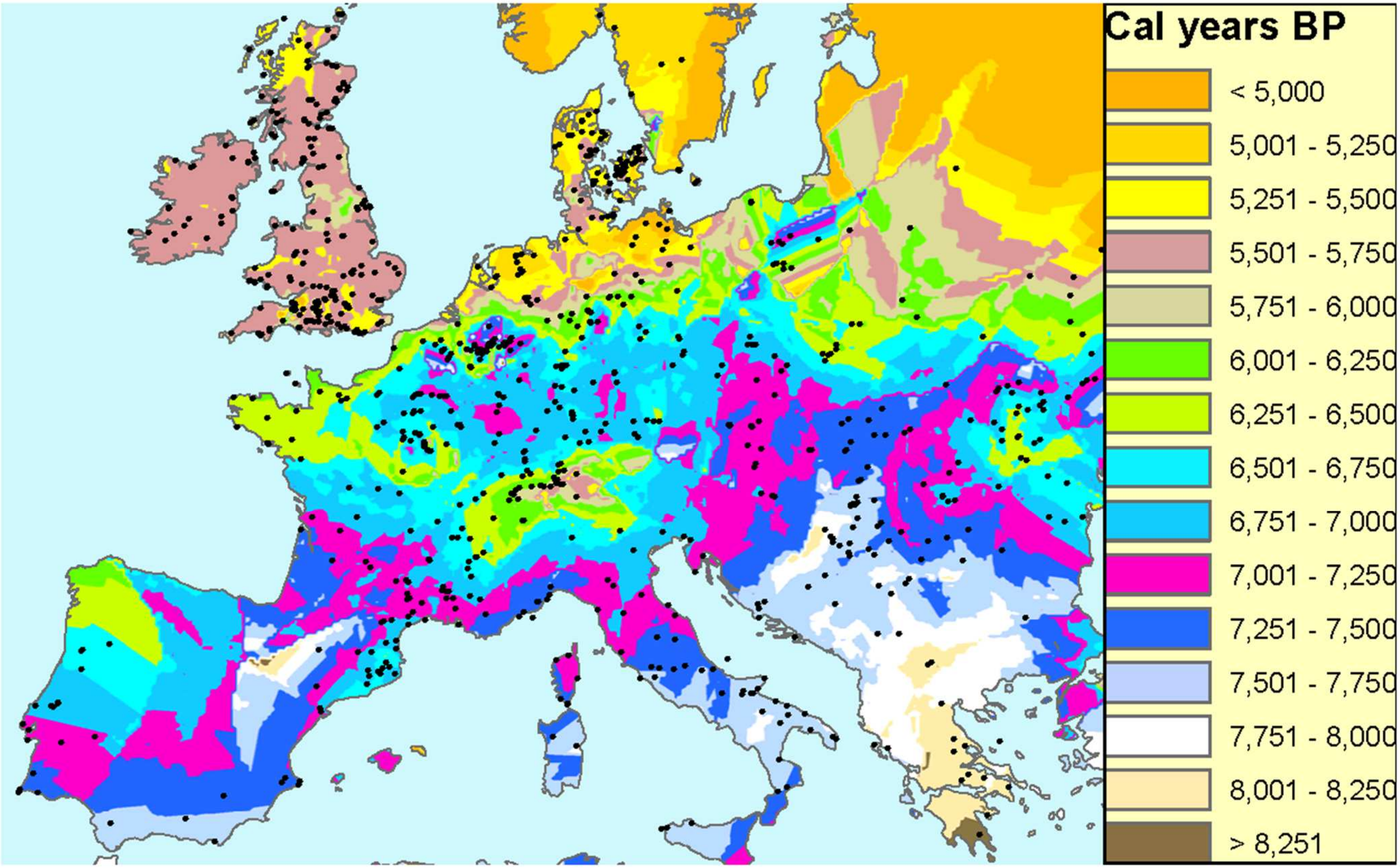

$C < 3$, so less than 3 HGs were converted per F per generation

Fort, *PNAS* (2012)

Cultural effect (%) = (speed – demic speed) /speed · 100

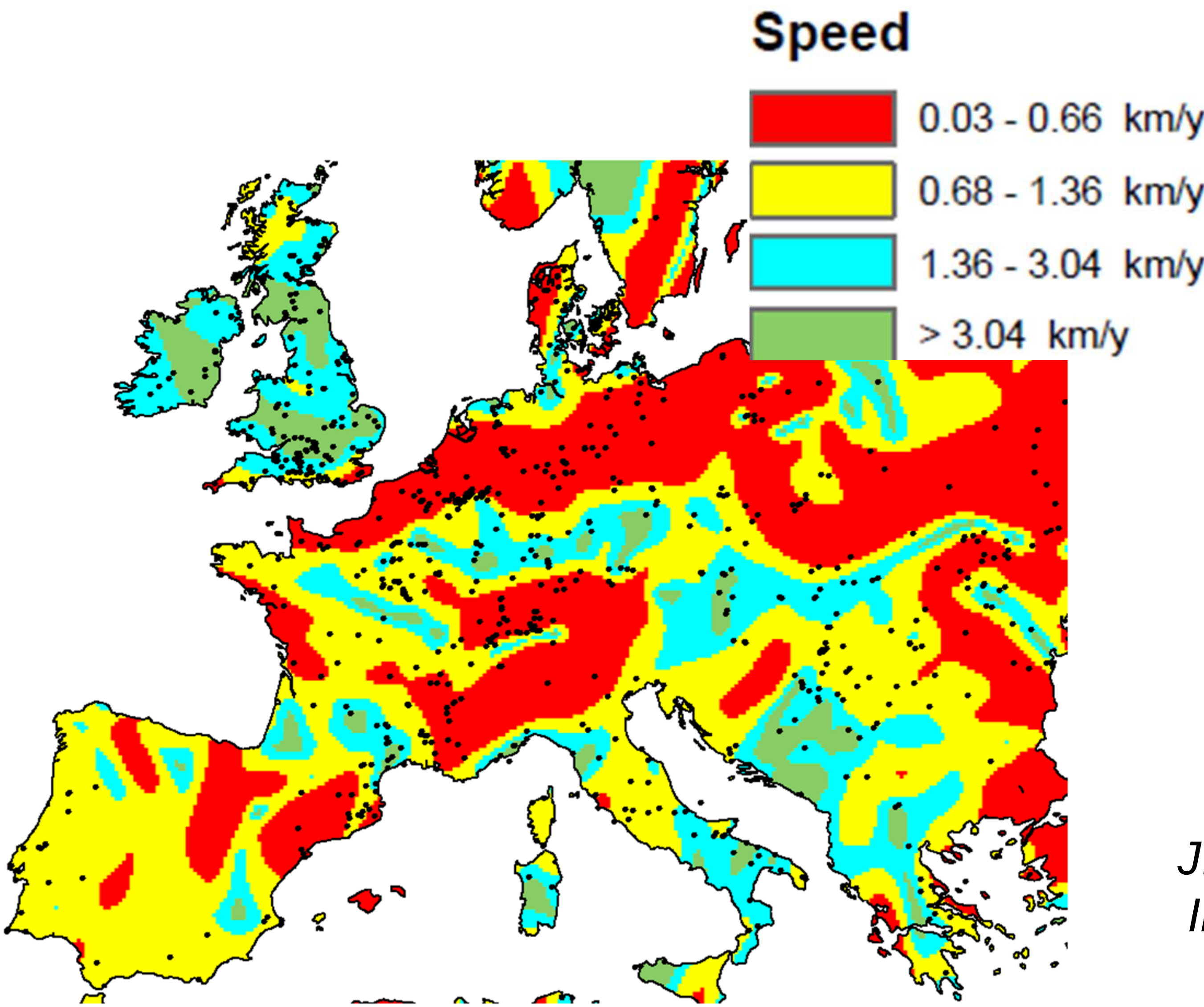



Fort, *PNAS* (2012)



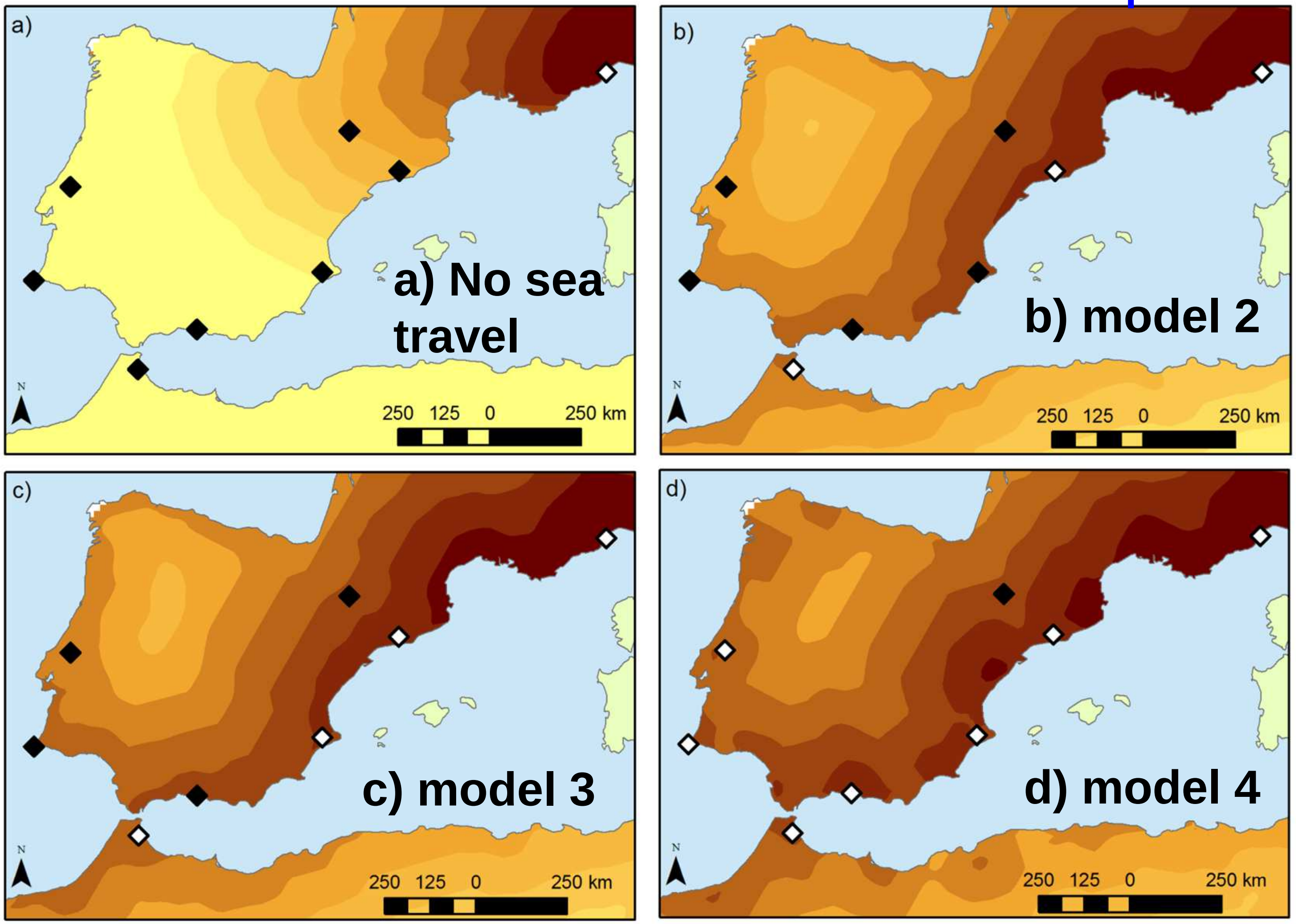

Fort, *J. R. Soc. Interface* (2015)

*Database from Fort, Pujol & vander Linden, Amer. Antiq. (2012)*




Fort,
*J. R. Soc. Interface*
(2015)

# WEST MEDITERRANEAN: oldest site per region



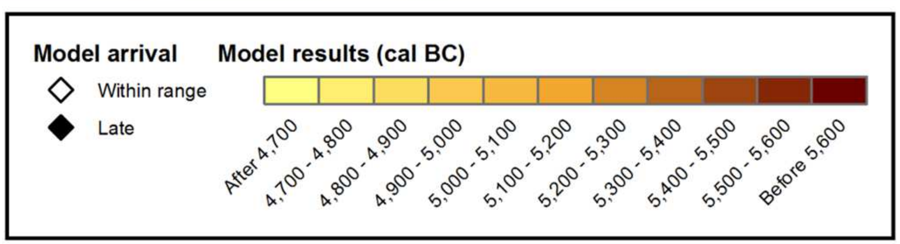

**b)-d) Sea travel up to 350 km**

**b) preference for closer destinations**

**b) all distances within 350 km equally likely**

**b) all jumps of 350 km**

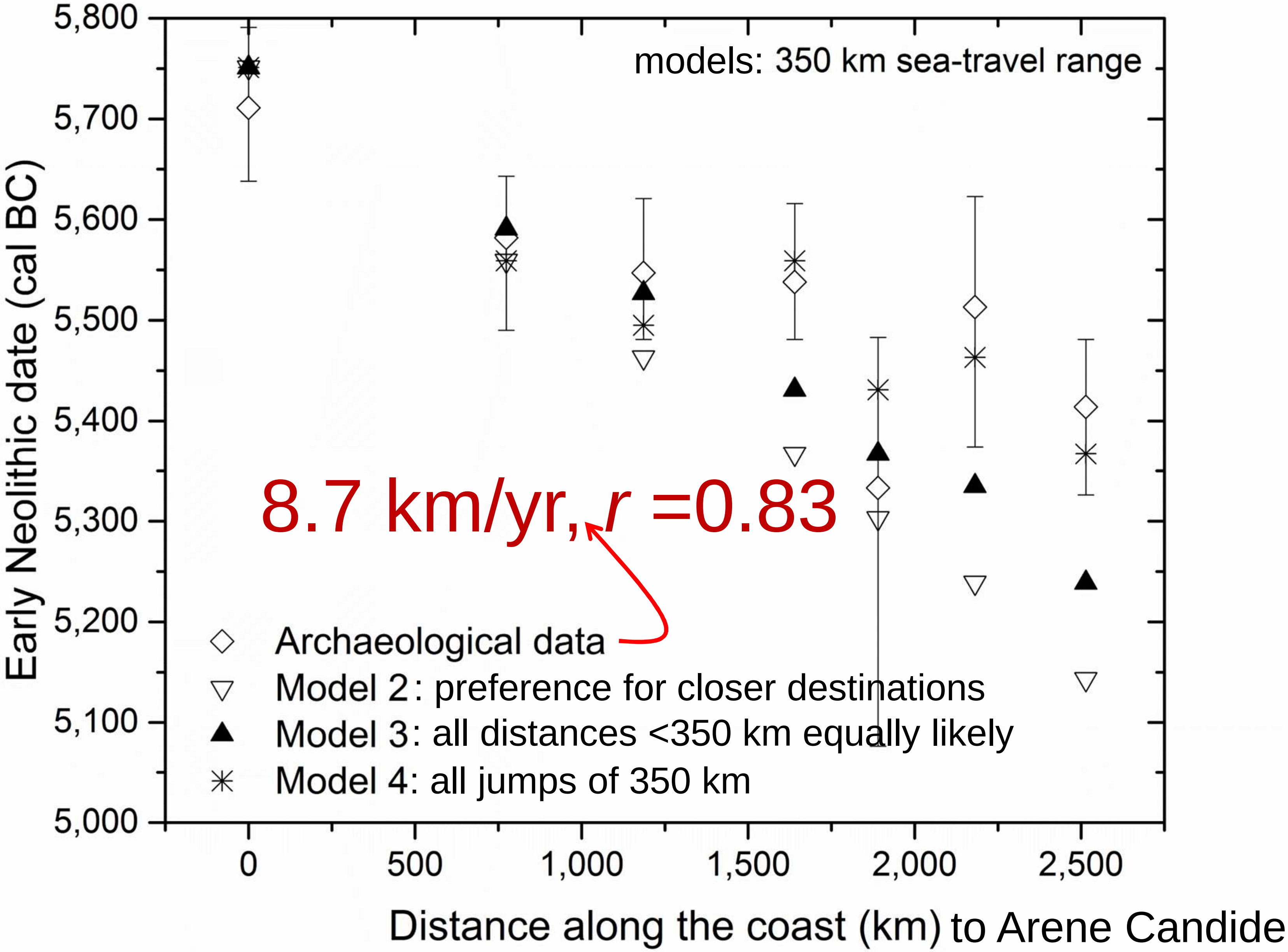
**Isern, Zilhao, Fort & Ammerman, *PNAS* 2017**




**◇ within range**

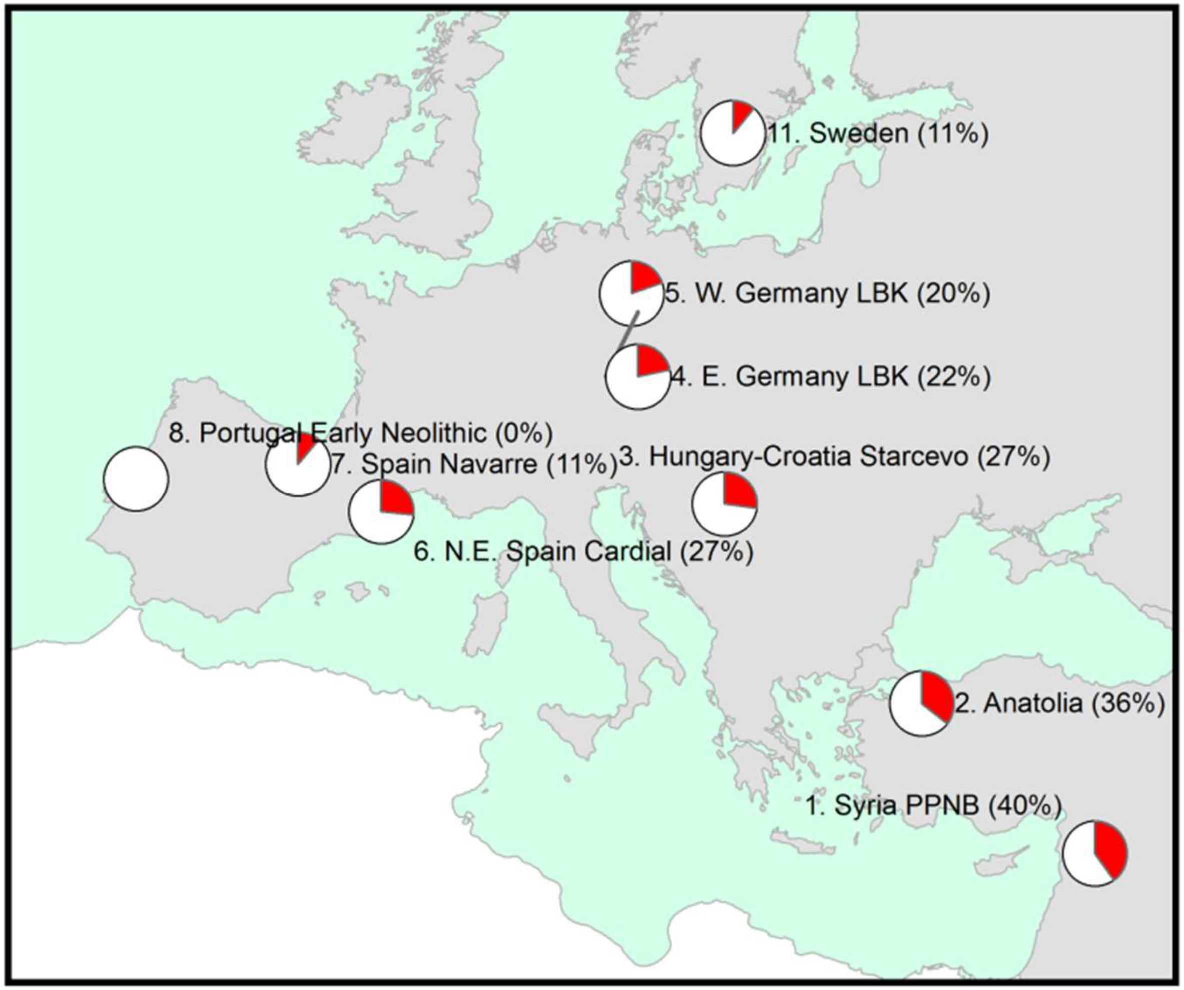
**◆ too late**

# WEST MEDITERRANEAN: oldest site per region

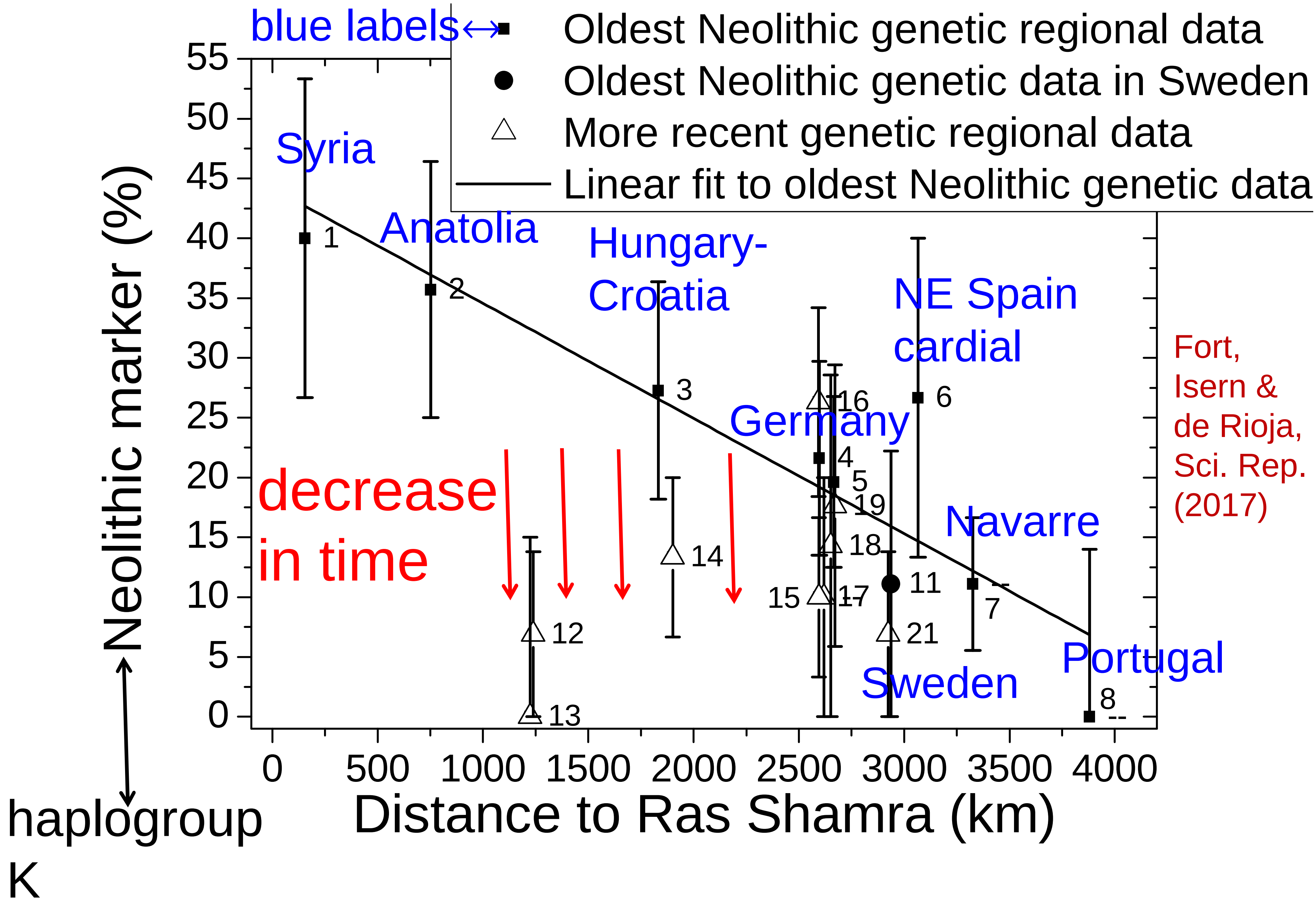


# Ancient genetics

We have gathered a database of all Neolithic individuals (513) whose mtDNA has been determined




We analyze haplogroup K because its frequency (red) decreases Westwards and Nothwards in farmers (and is absent in HGs). We expect that cultural transmission can cause this.



blue labels↔
Oldest Neolithic genetic regional data
Oldest Neolithic genetic data in Sweden
More recent genetic regional data
Linear fit to oldest Neolithic genetic data
Syria
Anatolia
Hungary-Croatia
NE Spain cardial
Germany
Navarre
Sweden
Portugal
decrease in time
Fort, Isern & de Rioja, Sci. Rep. (2017)
Neolithic marker (%)
Distance to Ras Shamra (km)
haplogroup K

# Simulations

Simulations begin with some farmers only at Ras Shamra, the oldest PPNB site in Syria in Pinhasi et al (2005), at the date reported there (8,233 cal yr BC).

We set the initial %K at the cell containing Ras Shamra by trial and error, so that the simulation yields the observed %K at the average location and date (7,258 cal yr BC) of the 15 early farmers in Syria whose mtDNA is known.

All other grid cells are initially empty of farmers and with HGs at their saturation density.

# Simulations

Each node of the grid is classified as inland, coast, mountain or sea.
At each node in the grid and time step (1 generation=32 yr), we compute 3 processes:

(1) Inland dispersal of farmers between neighbor cells with side 50 km and probability=62% (both values from ethnographic data).

Sea travel of farmers up to 150 km (so the arrival times agree with the archaeological data on average for the East+West Mediterranean).

(2) Cultural transmission: next slide.
(3) Reproduction: next slide.

# Simulations

(2) Cultural transmission:

$P_N$ =farmers who *have* haplogroup K.

$P_X$ = farmers who *do not have* haplogroup K.

$P_{HG}$ = hunter-gatherers (no HG has haplogroup K).

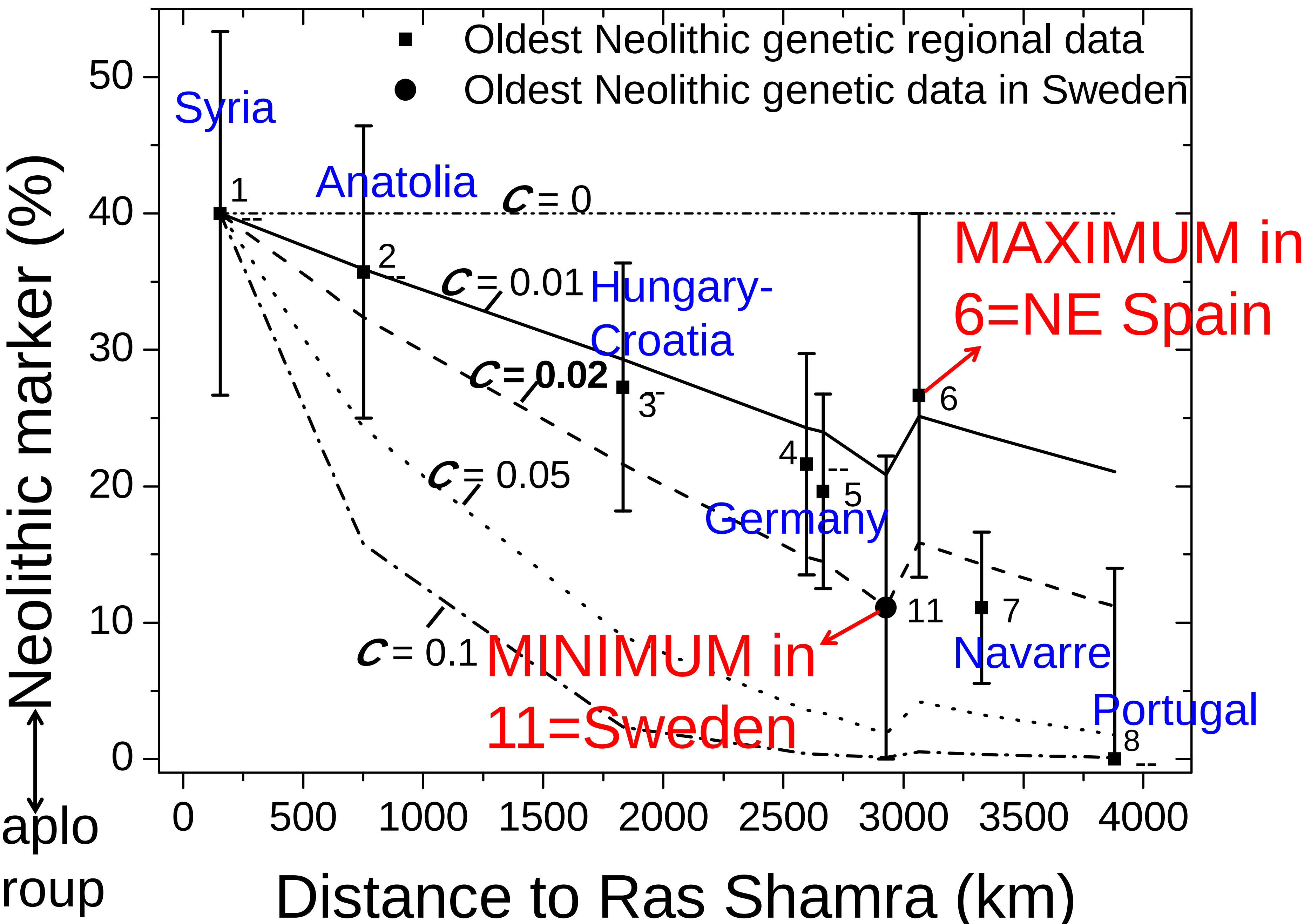
$$\%K = \frac{P_N}{P_N + P_X}$$

Cultural transmission theory (Cavalli-Sforza & Feldman 1981; Fort 2011, 2012): $couples\ HN = C\frac{P_{HG}P_N}{P_{HG}+P_N+P_X}$

$$couples\ HX = C\frac{P_{HG}P_X}{P_{HG}+P_N+P_X}$$

random mating for farmers $\rightarrow couples\ NX = \frac{P_N P_X}{P_N + P_X}$

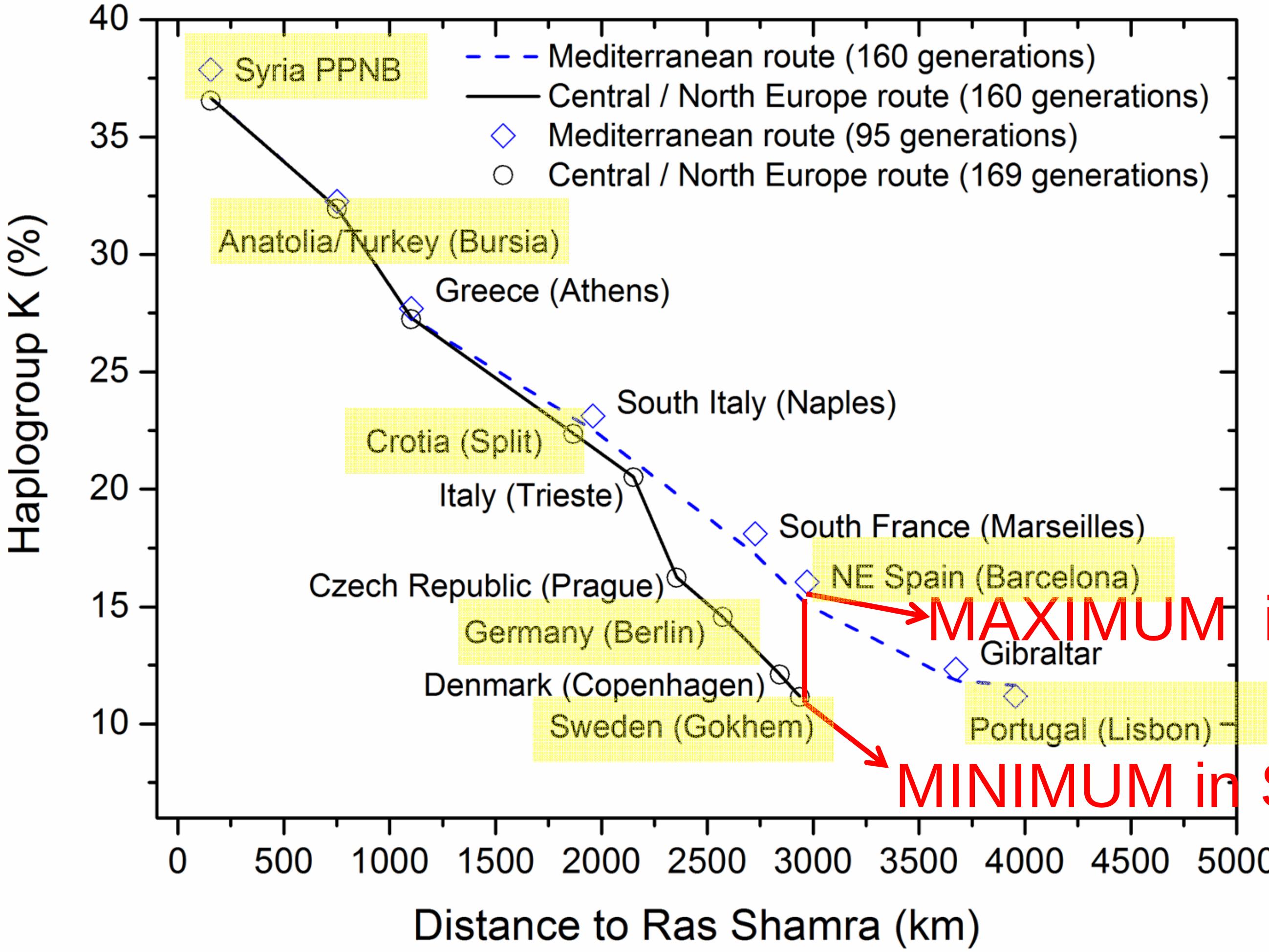
(3) Reproduction: each couple of farmers has 2Ro children (Ro=2.45). HGs have Ro=1 (steady state). For 50% of mixed matings (HN and HX), children are X.




haplo
group
K

Fort, Isern & de Rioja, Sci. Rep. (2017)

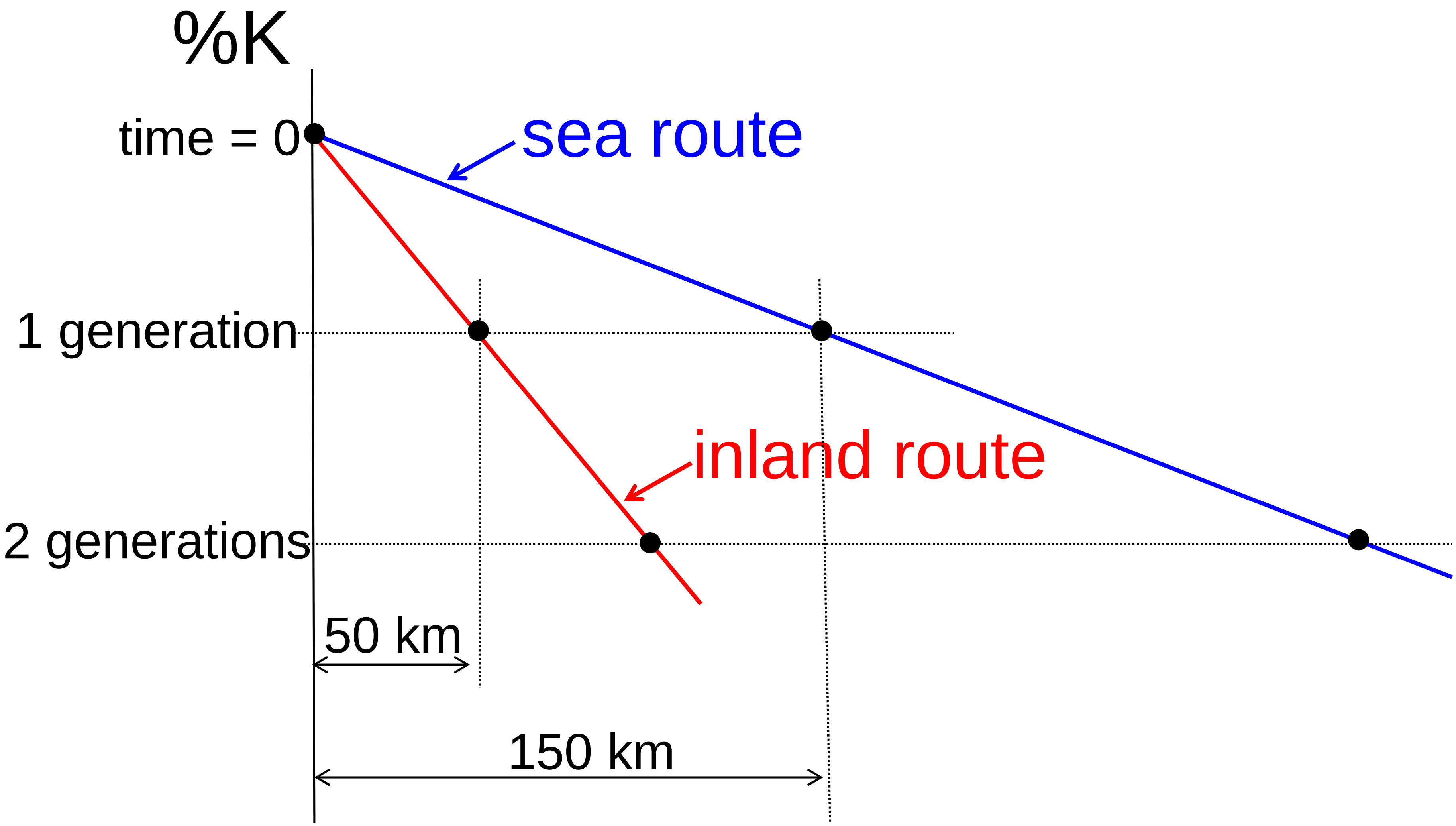
# Why is there a minimum in Sweden?
# Why is there a maximum in NE Spain?




yellow indicates locations that appear in the previous slide

Why is the inland cline steeper than the Mediterrean cline?

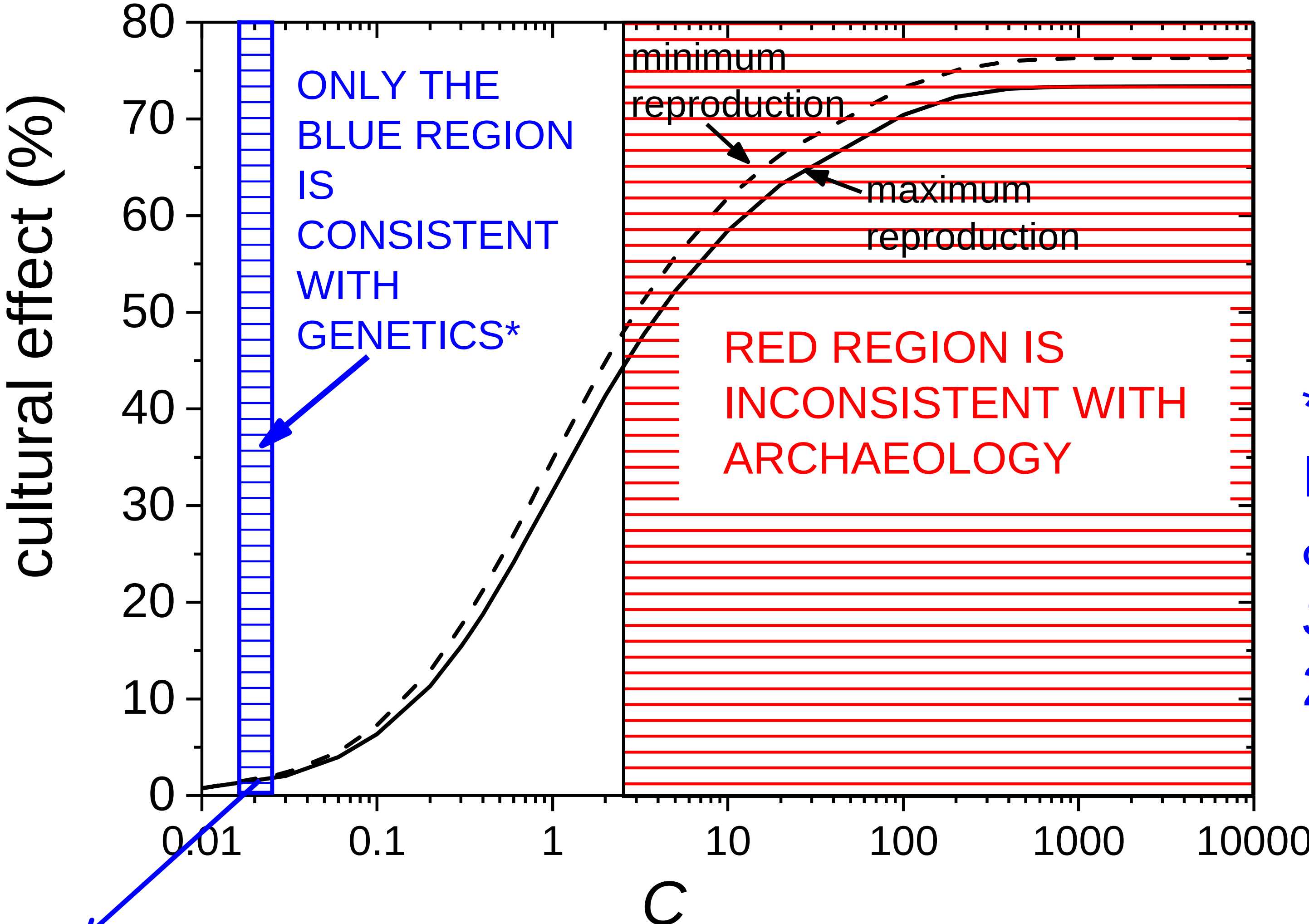
## Why is the inland cline steeper than the Mediterrean cline?




This explains the minimum and maximum.

It is also a genetic confirmation that sea jumps were longer.

Effect (%) = (speed – demic speed) /speed · 100




*Genetics: Isern, Fort & Rioja, *Sci. Rep.* 2017

- cultural effect of only 2%, so demic>>cultural.
- $C$=0.02, so only 2% farmers in cultural diffusion.