

# An ABM approach to the Neolithic spread in Europe and an ancient genetic cline

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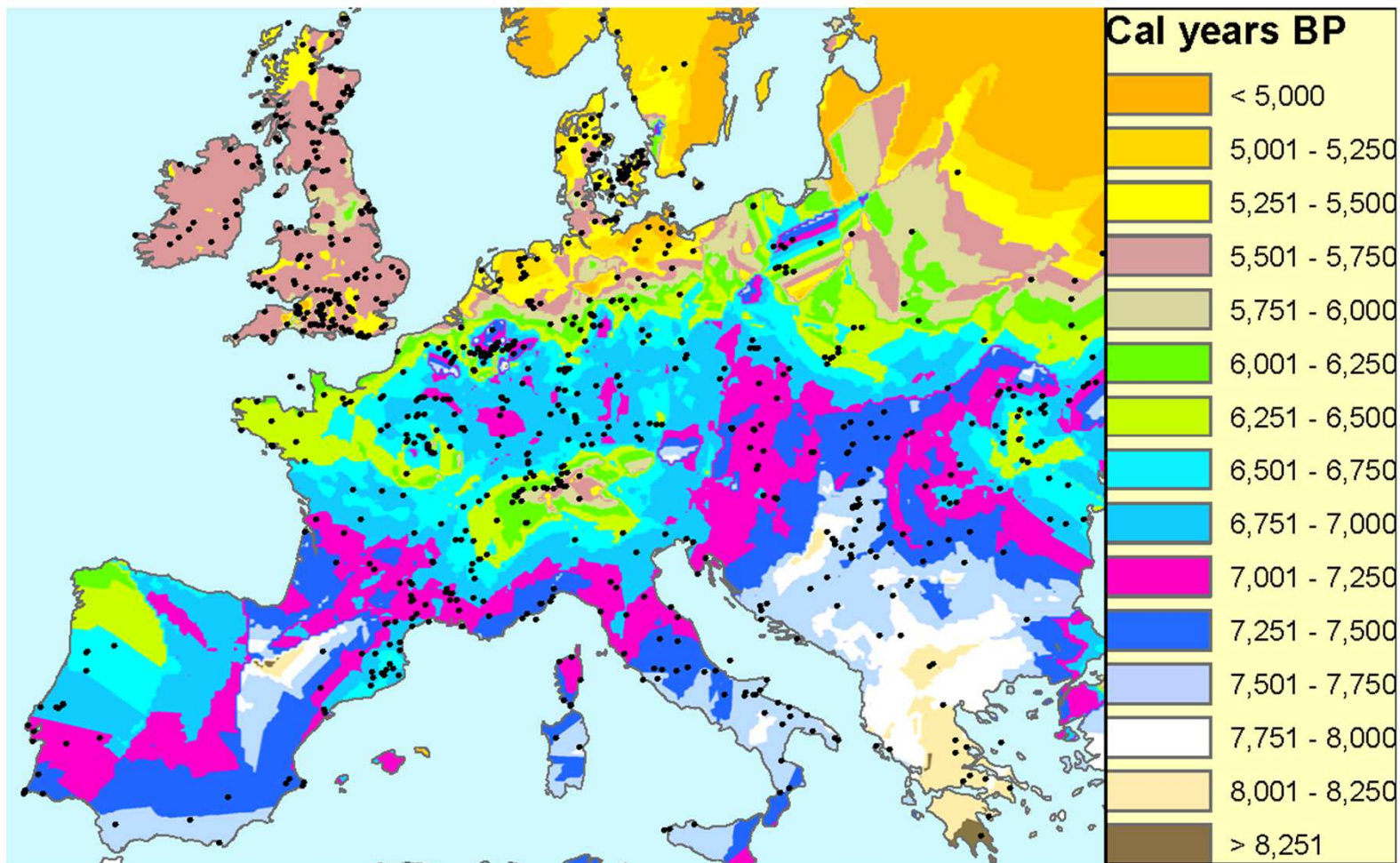


MCIN/AEI/10.13039/501100011033 (grant PID2019-104585 GB-I00)



# Archaeology

- Neolithic = farming and stockbreeding
- It replaced the Mesolithic (hunting and gathering)
- The oldest Neolithic sites are in the Near East:

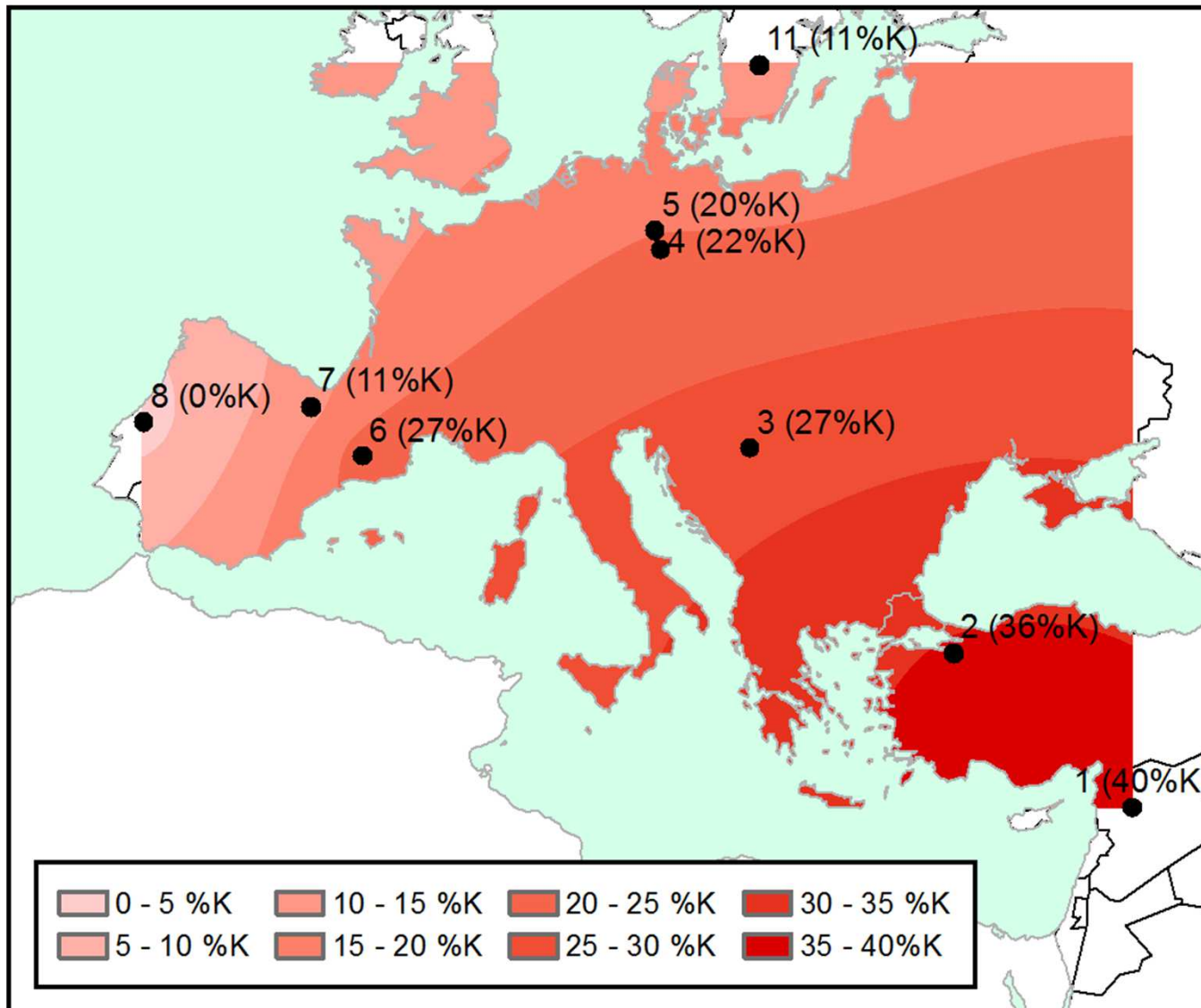


interpolation  
map  
from  
Fort,  
*J. R. Soc.  
Interface*  
(2015)



# Ancient genetics

mtDNA haplogroup K: absent in hunter-gatherers



**This  
pattern  
(cline)  
suggests  
interbreeding**

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



# Simulations

Grid of square cells. Initially farmers only at the cell containing the oldest site in Syria (Abu Hureyra) with a %K such that we obtain the observed %K (40%) 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.

At each node in the grid and time step (1 generation=32 yr), we compute 3 processes:

- (1) **Dispersal** (38% do not migrate, from ethnography)
- (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 (all without haplogroup K).

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

Cultural transmission theory (Cavalli-Sforza & Feldman 1981;

Fort 2011, 2012):  $\text{couples } HN = \eta \frac{P_{HG}P_N}{P_{HG} + P_N + P_X}$

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

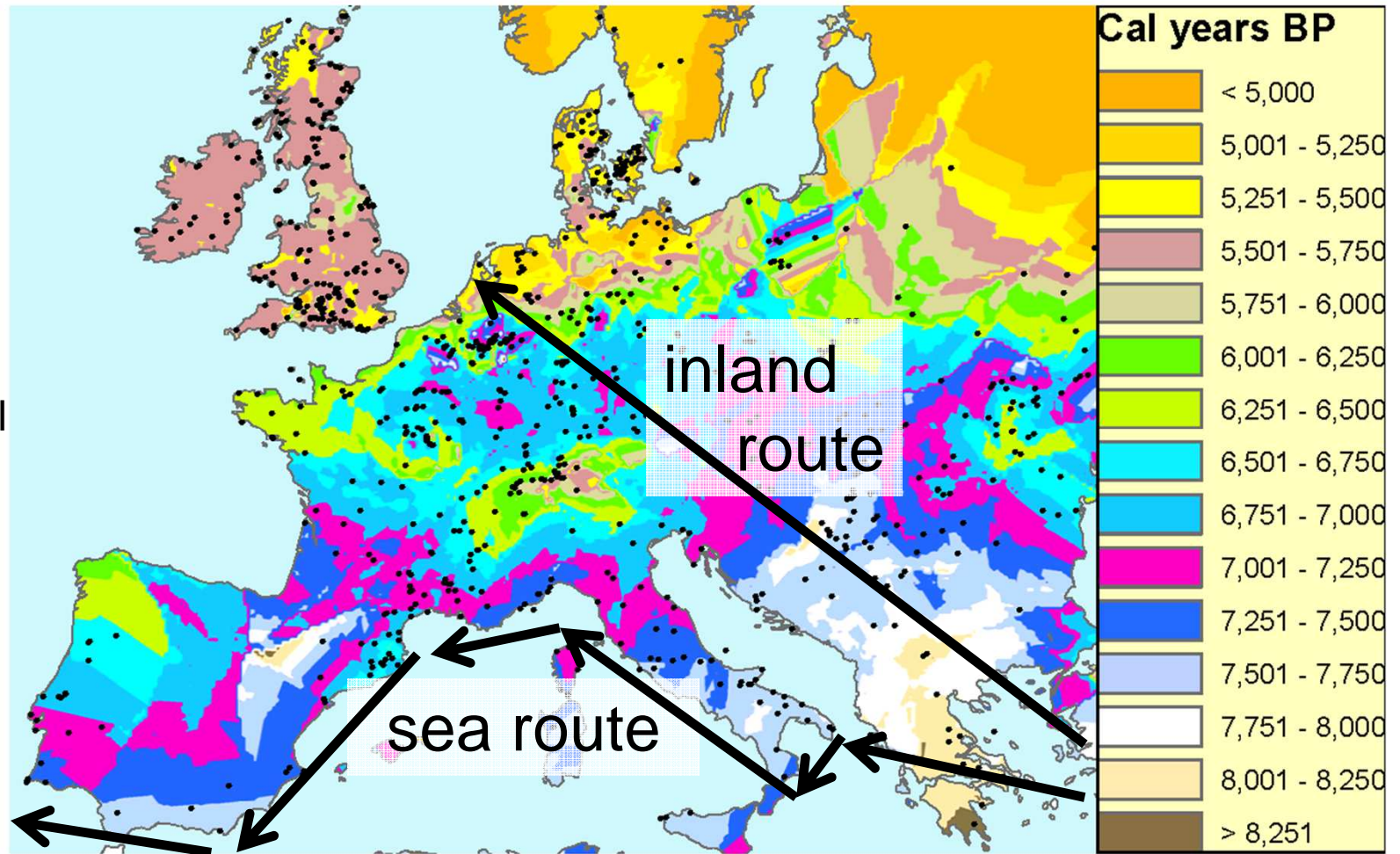
random mating for farmers  $\rightarrow$   $\text{couples } NX = \frac{P_N P_X}{P_N + P_X}$

(3) **Reproduction:** each couple of farmers has  $2R_o$  children ( $R_o=2.45$ ). Genetically mixed matings (HN and NX) have 50% children N and 50% children X.



# Two routes

interpolation  
of  
archaeological  
dates  
from  
Fort,  
*J. R. Soc.  
Interface*  
(2015)



Now (year 2021) we have ancient genetic data for both routes



# Distances

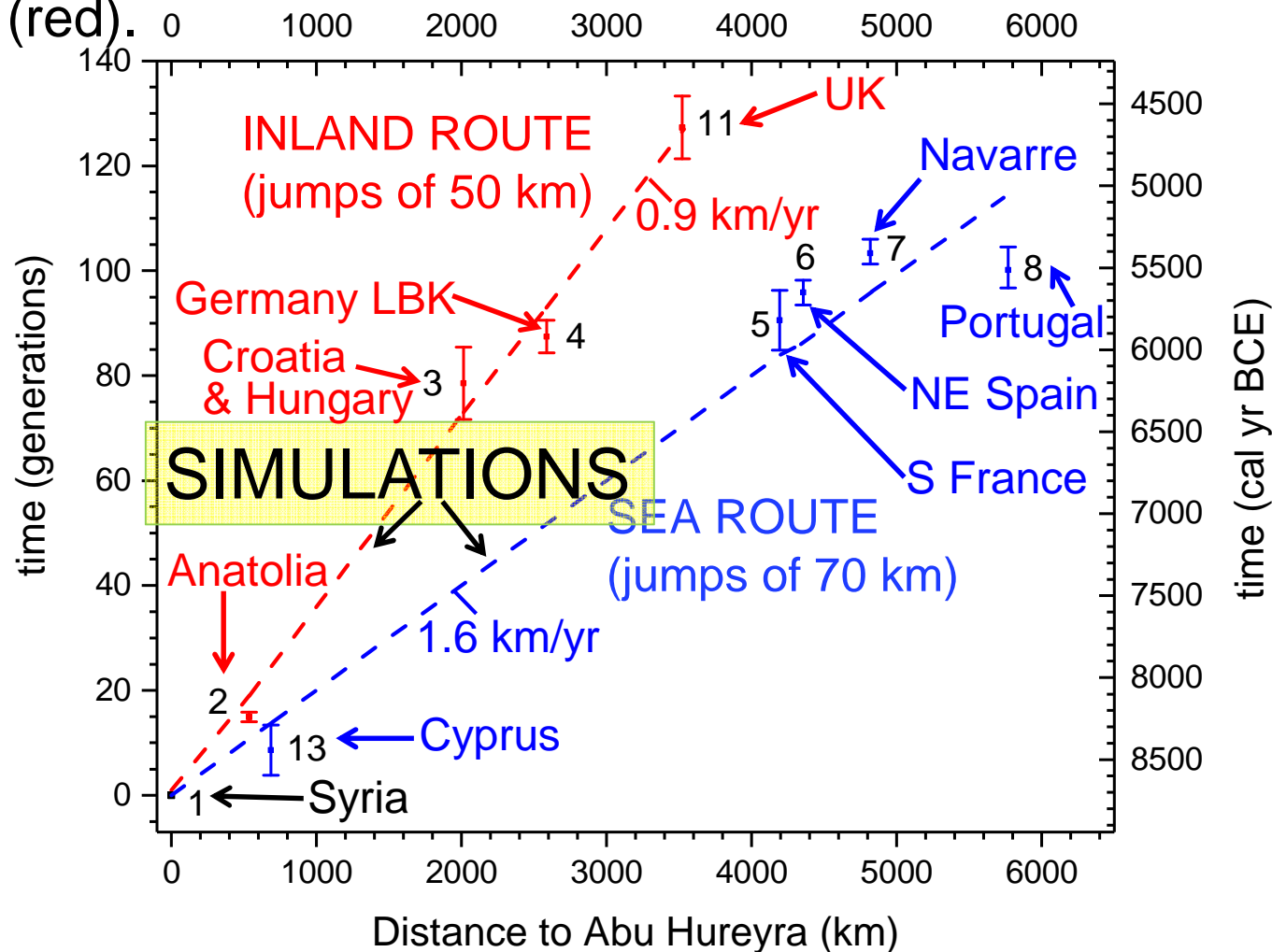
(1) Inland route: great circles = 'straight lines'

(2) Sea route: [sea-seek.com](http://sea-seek.com). Example:



# Simulations + archaeological data

Initially there are farmers only at the cell with the **oldest PPNB site in Syria (Abu Hureyra, <9,038 cal BC)** at a date (8,718 cal BC) such that the simulations agree with the data along the inland route (red).



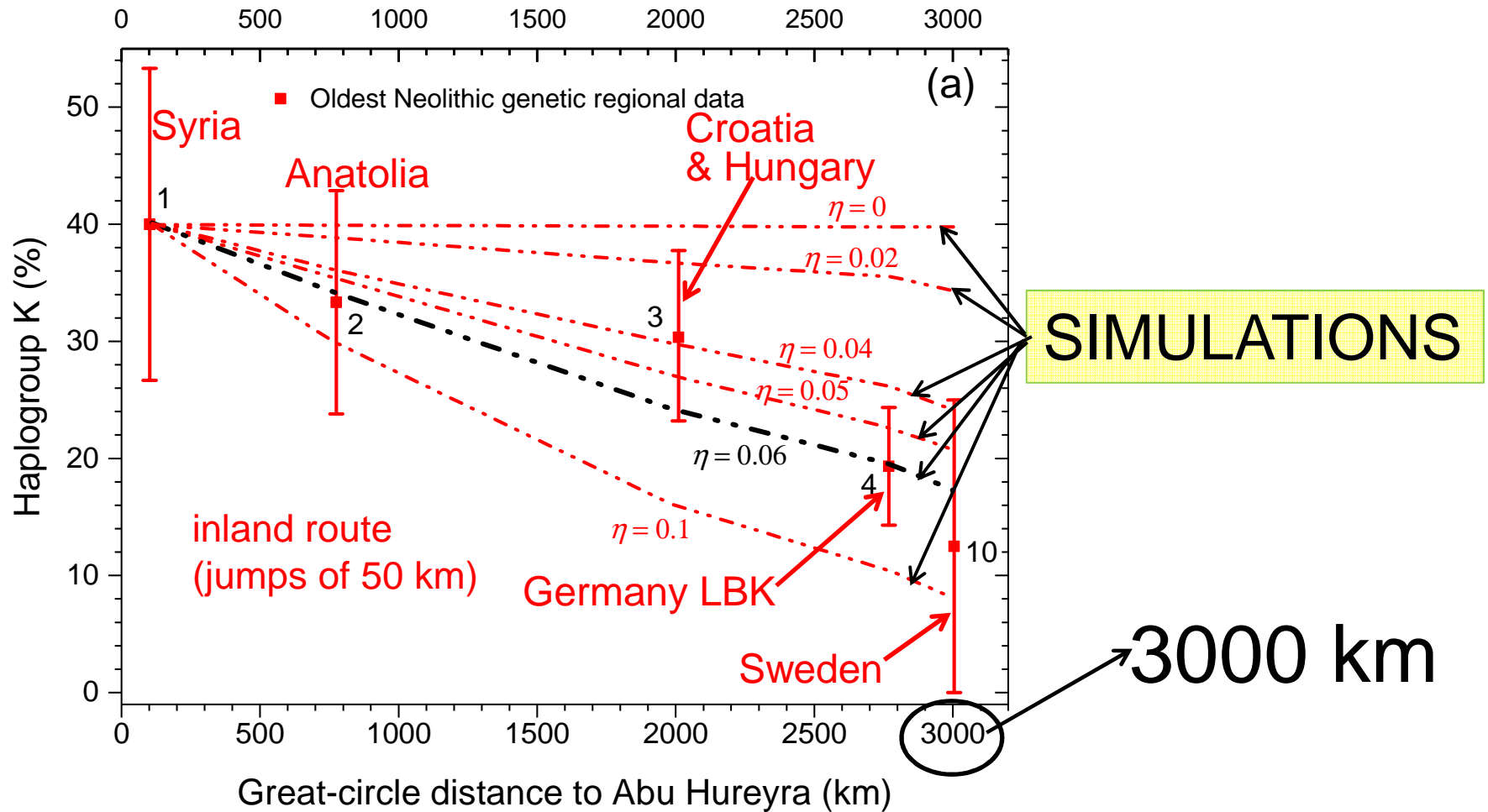
Inland route:  
simulations  
with jumps of  
50 km per  
generation  
(value from  
ethnography)

Sea route:  
best fit for  
simulations  
with jumps of  
70 km





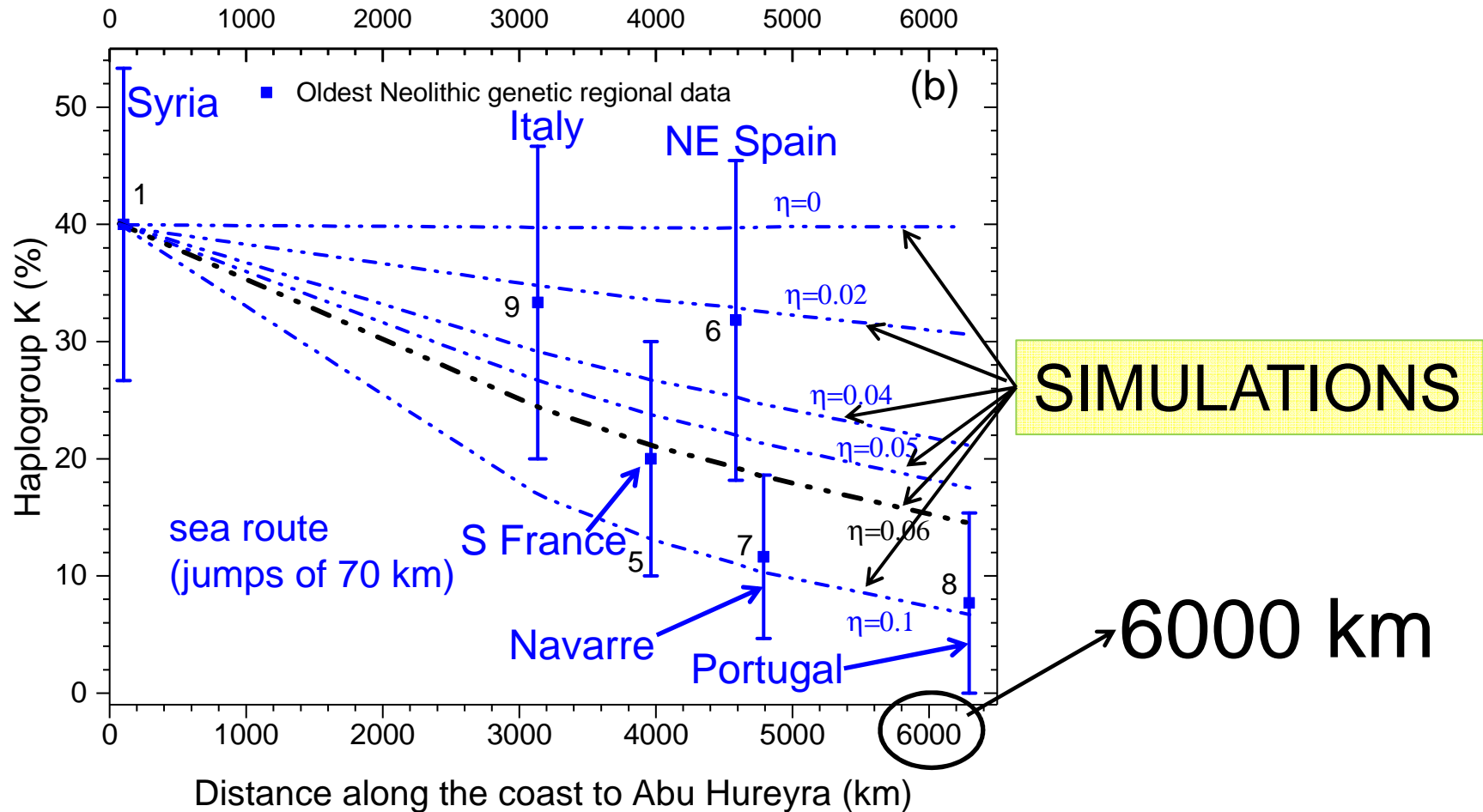
# Inland genetic cline



**Best fit:  $\eta = 0.06$**



# Mediterranean genetic cline



**Best fit:  $\eta = 0.06$  again!**



# Two routes, two clines

route	slope of cline	interbreeding ( $\eta \cdot 100$ )
inland (jumps of <u>50 km/gen</u> )	8 %K / 1,000km	6% of early farmers ( $\eta = 0.06$ )
Mediterranean (jumps of <u>70 km/gen</u> )	4 %K / 1,000 km	6% of early farmers ( $\eta = 0.06$ )



# Conclusions

The dispersal behavior depends on geography:

-early farmers moved longer distances per generation along the sea route.

In turn this led to:

-a faster spread rate along the sea route,

-a lower slope of the genetic cline along the sea route (due to less interbreeding events per unit distance).

**In sharp contrast to this:**

The interbreeding and/or acculturating fraction of farmers (6%) was the same along both routes. **It did not depend on geography but only on the transition in the subsistence economy and its way of life.**

