



Computational modelling of Neolithic spread: archaeology and genetics

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The spread of the Neolithic in the Near East and Europe

We want to build a model that explains two kinds of data:

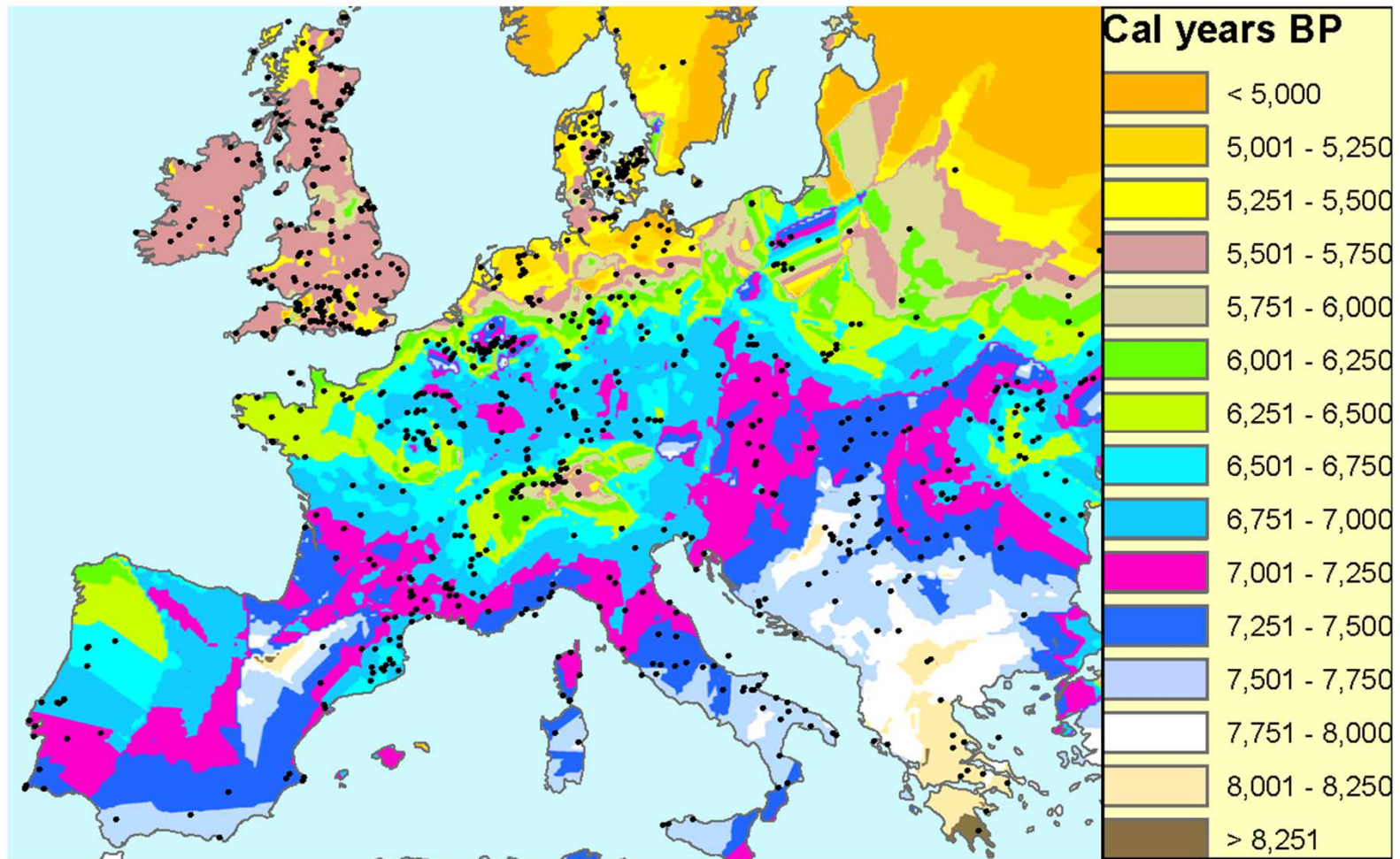
1) Archaeological data (slide 2)

+

2) Ancient genetic data (slide 3)



Interpolation of early Neolithic dates



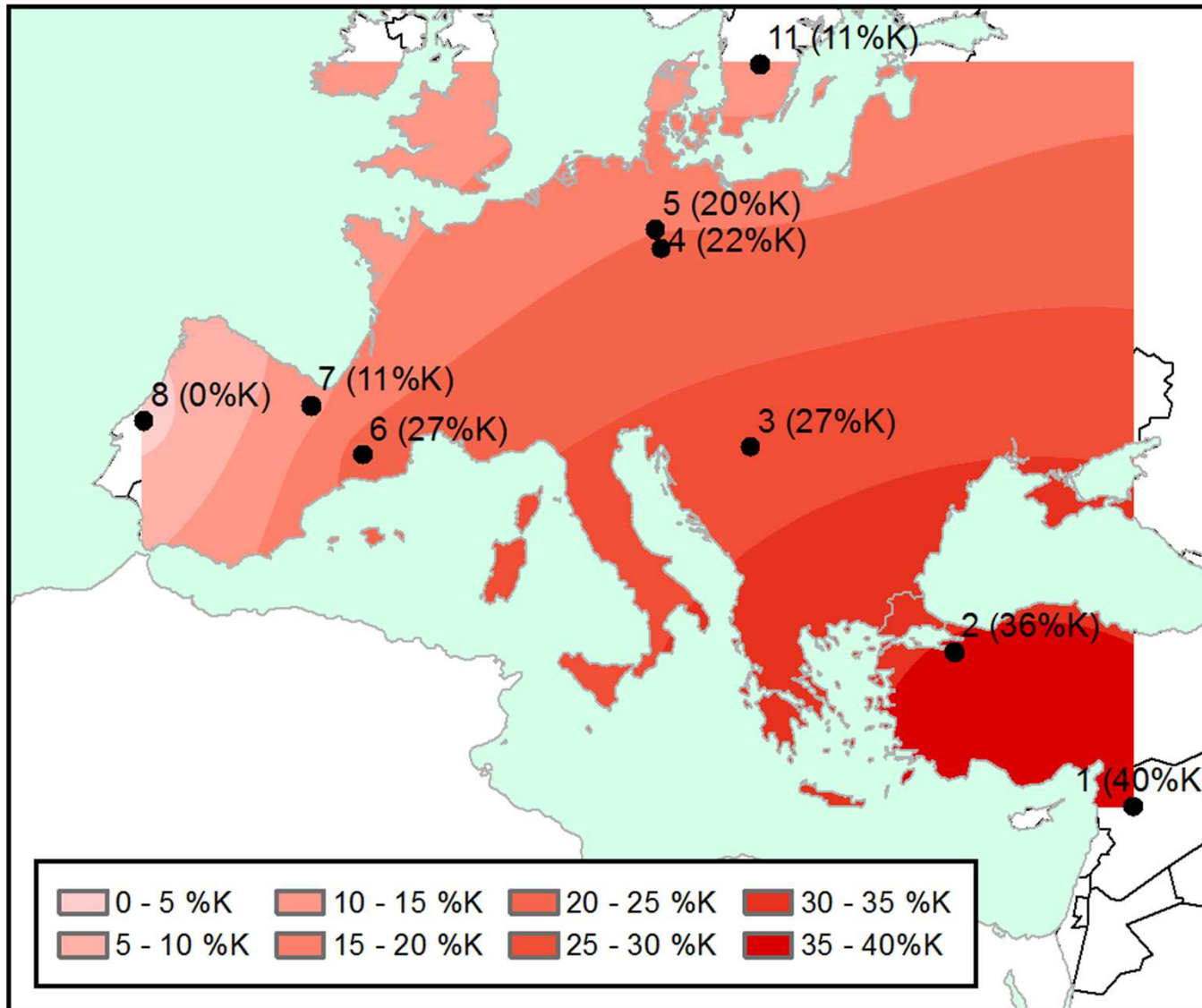
Fort, J. R. *Soc. Interface* (2015)

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



Ancient genetic data

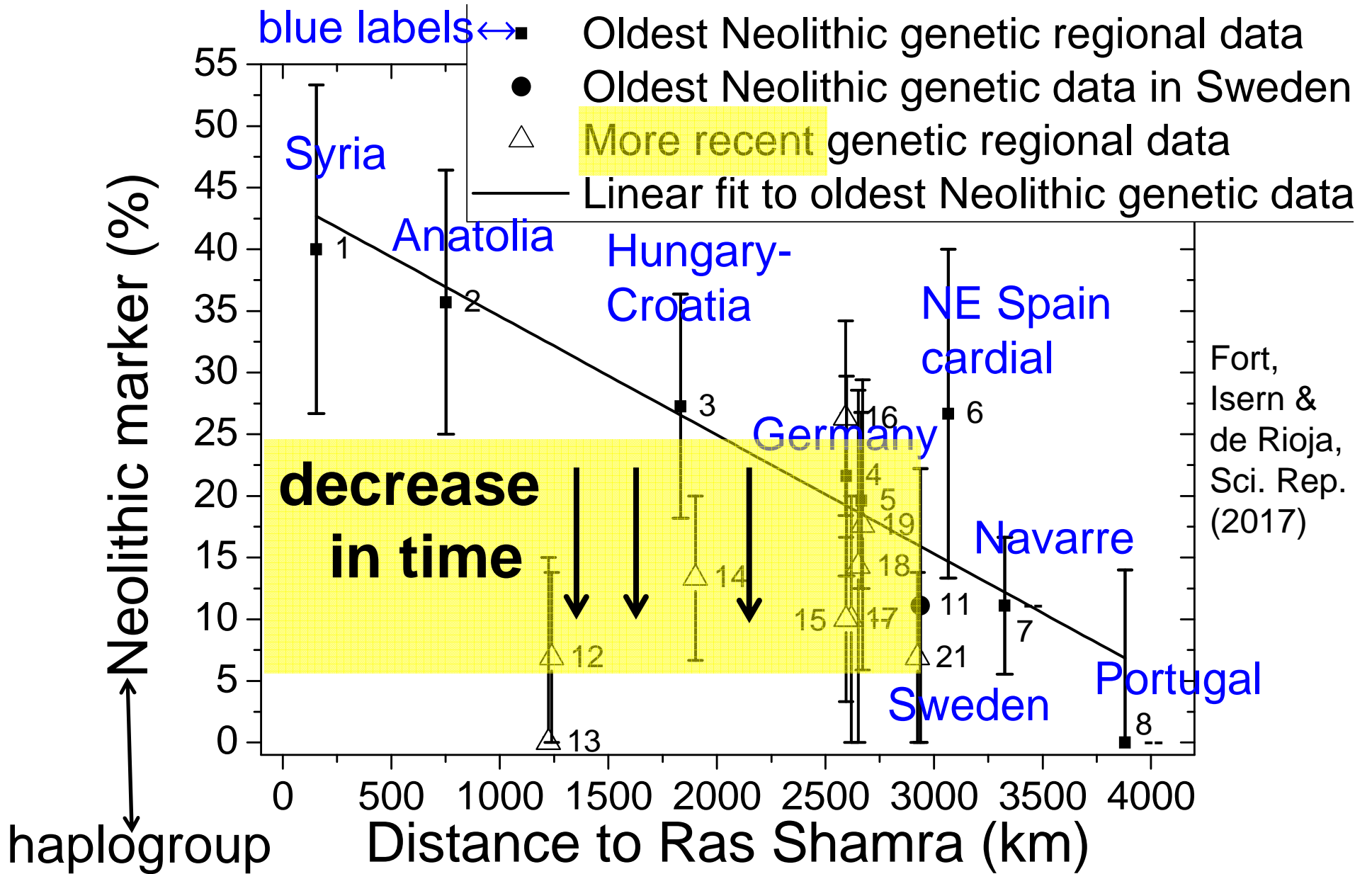
mtDNA haplogroup K: absent in hunter-gatherers



**This
pattern
(cline)
suggests
interbreeding**

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





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

This also suggests interbreeding



Ancient genetic data

Now (year 2021) we have ancient genetic data for more regions than in our previous work (Isern et al., 2017).

So now we have data for **two clines**:

-a cline for the inland route (Balkans, Germany...)

-a cline for the Mediterranean route (Italy, France...)



Simulations

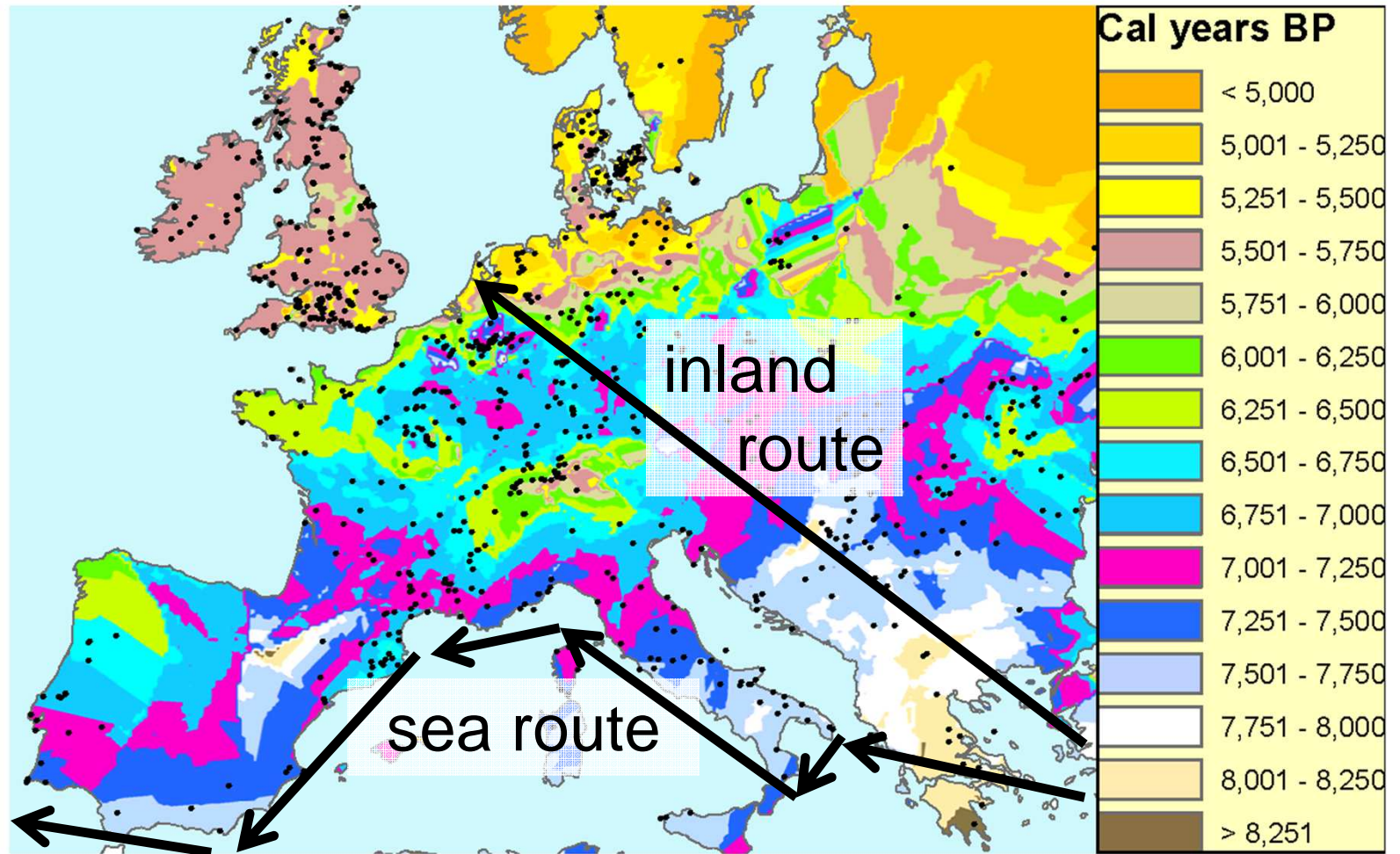
Rectangular grid of square cells.

Isern et al. (2017) used a real geography (i.e., with inland, coast and sea cells). Here we use a homogeneous geography (one grid for inland dispersal and another one for sea dispersal). Both approaches give almost the same results.

Isern et al. (2017) used non-integer population numbers. We use integer numbers. It is more reasonable biologically because, e.g., 1 or 2 individuals can jump to another cell, but not 1.5 or 1.7 individuals (as in Isern 2017).



Two routes



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. Example:



Details on the simulations

We set the initial %K at the cell containing Abu Hureyra by trial and error, until the simulation yields 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.



Details on the 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): $\text{couples } HN = \eta \frac{P_{HG} P_N}{P_{HG} + P_N + P_X}$

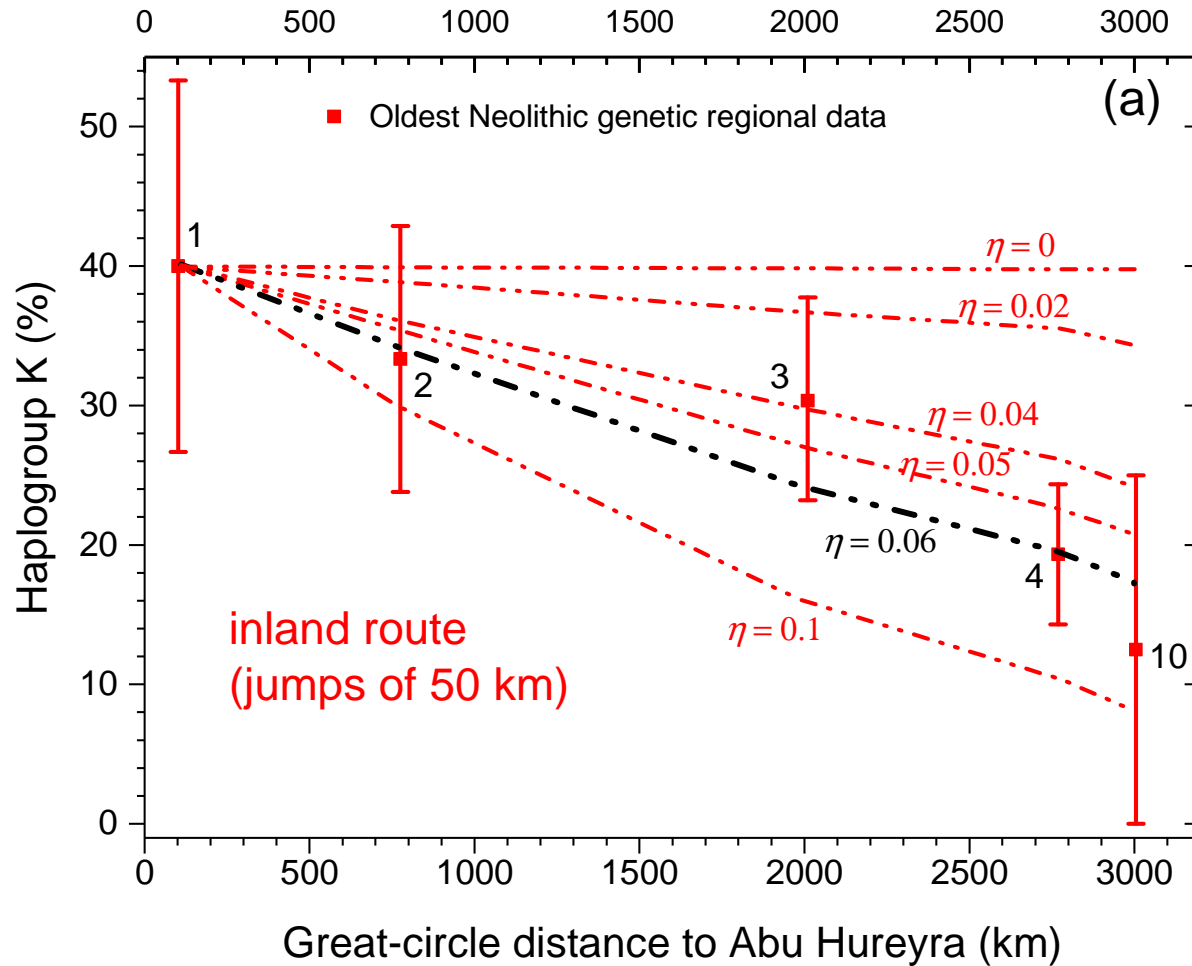
$$\text{couples } HX = \eta \frac{P_{HG} P_X}{P_{HG} + P_N + P_X}$$

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.



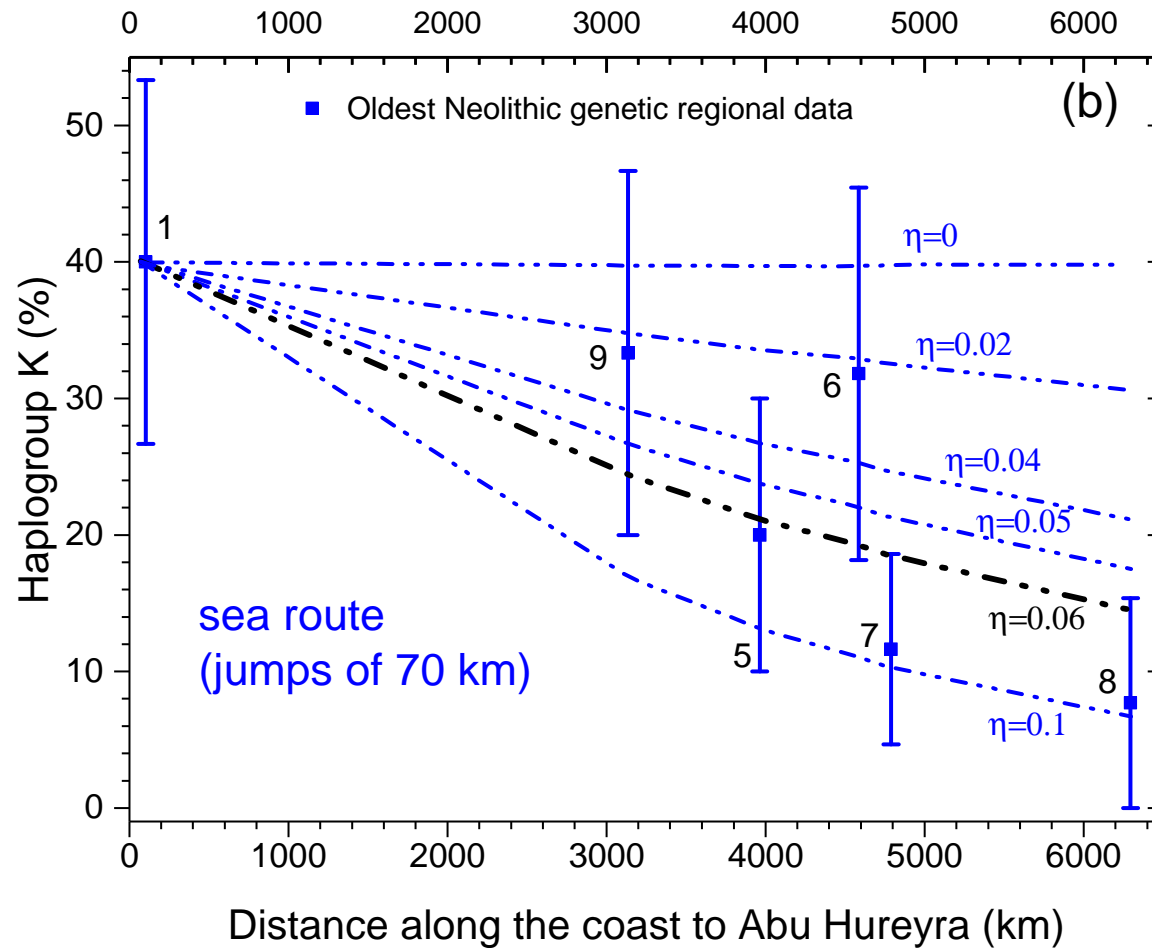
Inland genetic cline



Best fit: $\eta = 0.06$



Mediterranean genetic cline



Best fit: $\eta = 0.06$ again!



Two routes, two clines

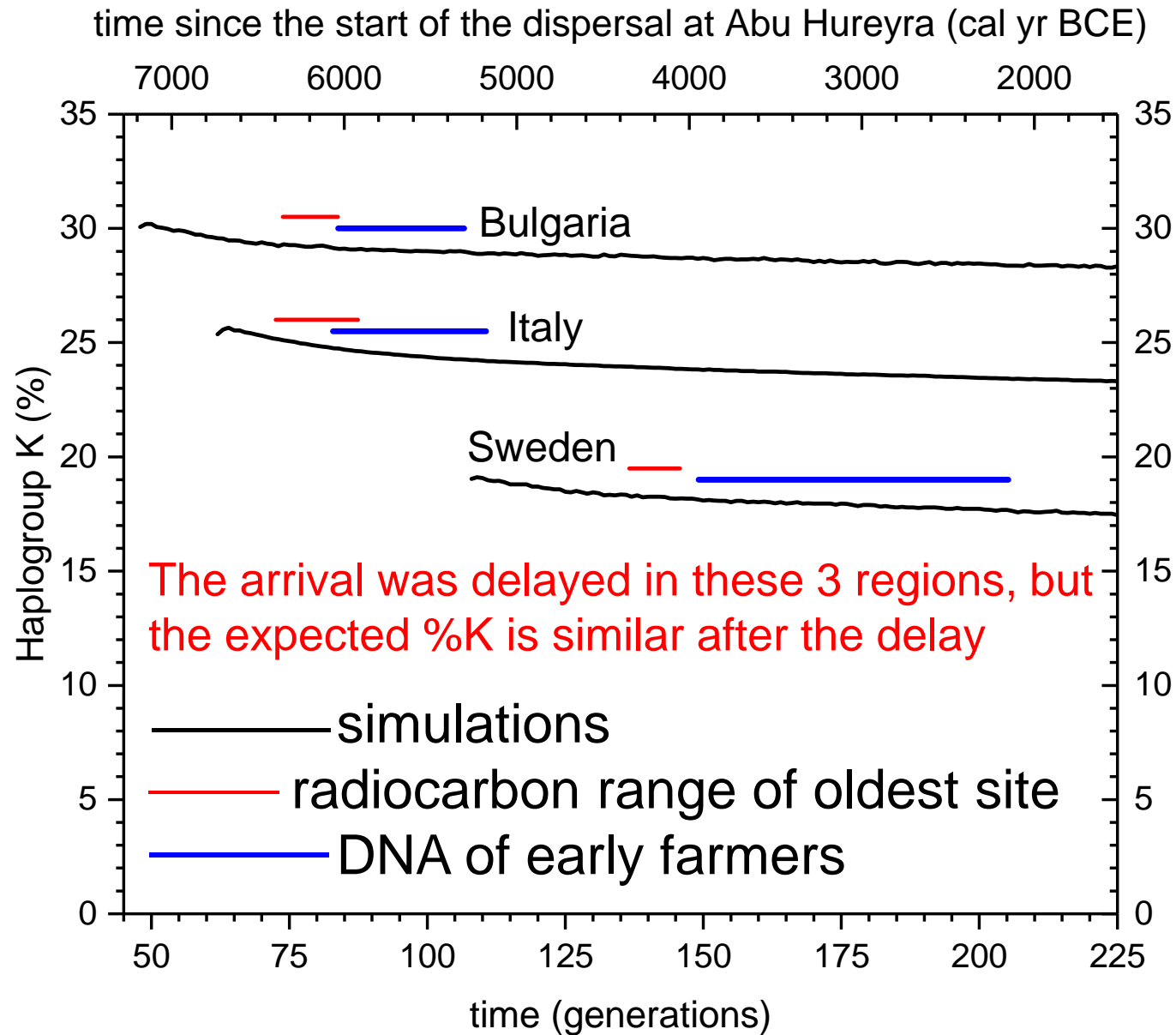
route	slope of cline	interbreeding ($\eta \cdot 100$)
inland (jumps of 50 km/gen)	8 %K / 1,000km	6% of early farmers
Mediterranean (jumps of 70 km/gen)	4 %K / 1,000 km	6% of early farmers

The dispersal behaviour depends on geography: it was very different. We know this from the archaeological data.

But the interaction between early farmers and hunter-gatherers (interbreeding) was strikingly similar (6%). We know this from the ancient genetic data (clines).



Delayed regions



Sensitivity analysis

We have analyzed the effects of:

- initial conditions: uncertainty of the initial %K (Syria)
- parameter values:
 - dispersal threshold
 - net fecundity of farmers
 - carrying capacity of farmers
 - carrying capacity of hunter-gatherers

The results are similar.

The conclusions do not change.



Conclusions

Geography was very important:

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

In turn this led to:

- faster spread rate along the sea route,
- 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.

