The spread of the Neolithic in Europe: an interdisciplinary approach

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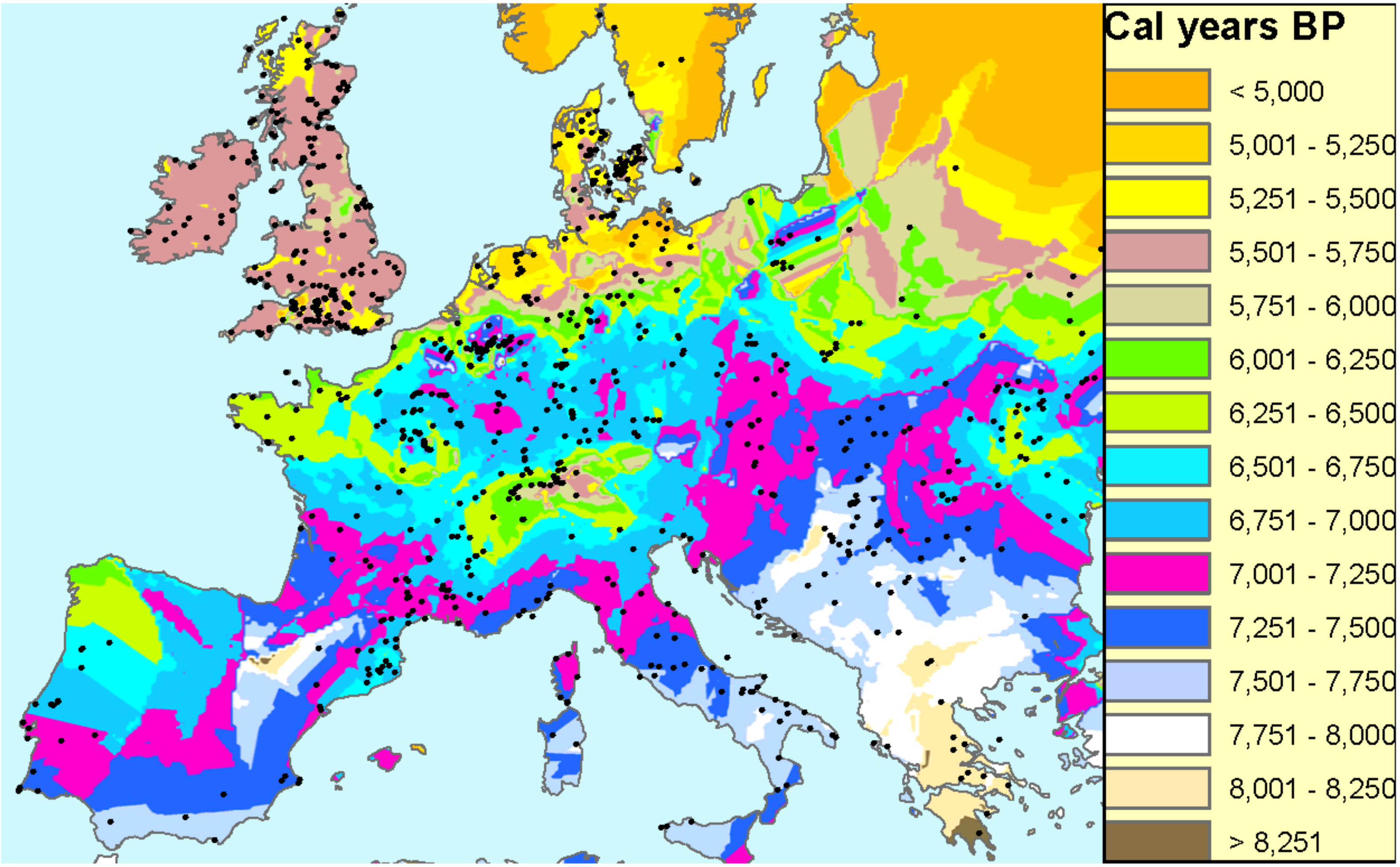
Archaeology

- 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)

Simulations

· Grid of square cells. Initially farmers only at the cell containing the oldest site in upper Mesopotamia (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 early farmers in upper Mesopotamia 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): $couples\ HN = \eta \frac{P_{HG} P_N}{P_{HG} + P_N + P_X}$

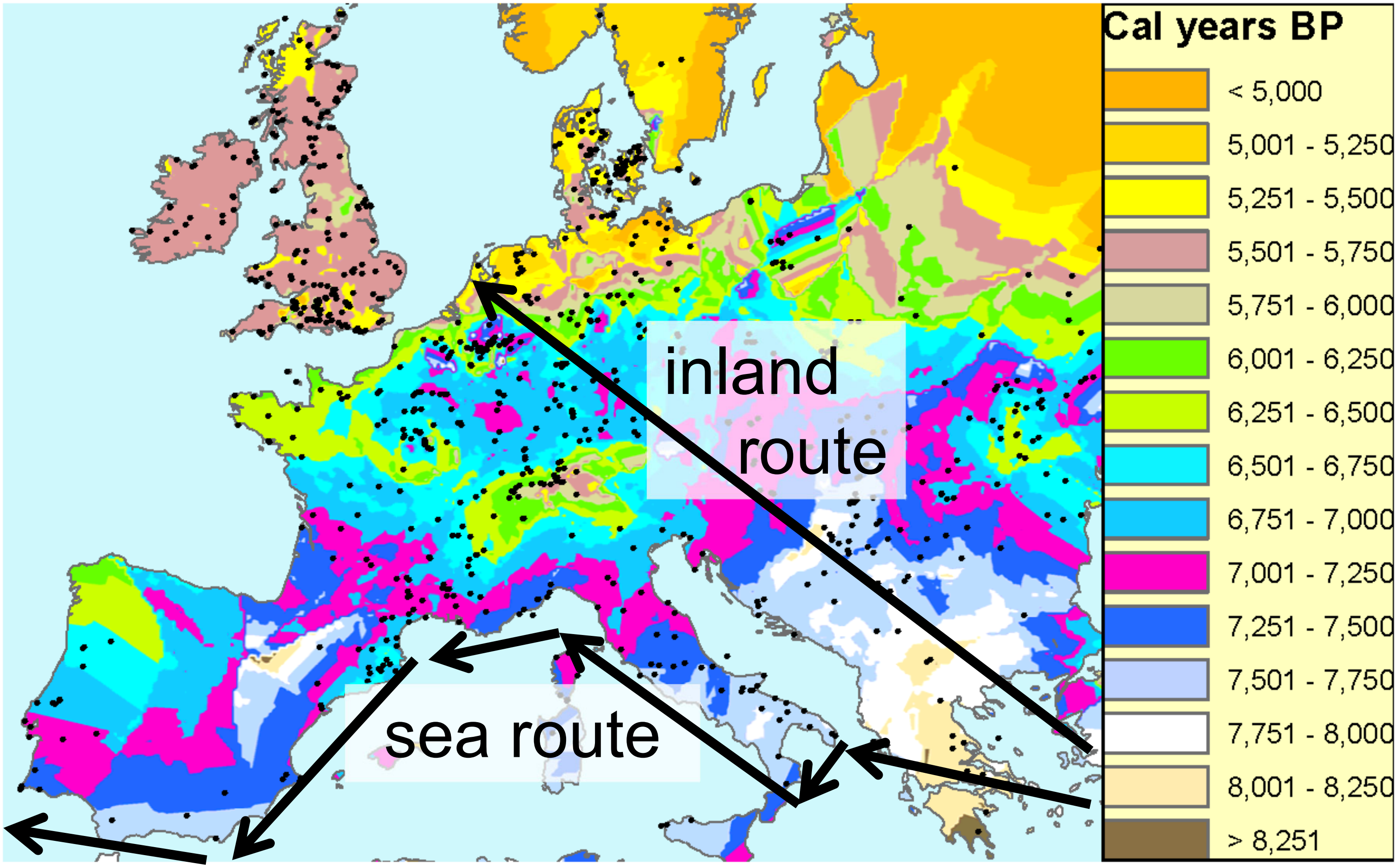
$$couples\ HX = \eta \frac{P_{HG} P_X}{P_{HG} + P_N + P_X}$$

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

(3) Reproduction: each couple of farmers has 2Ro children (Ro=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)

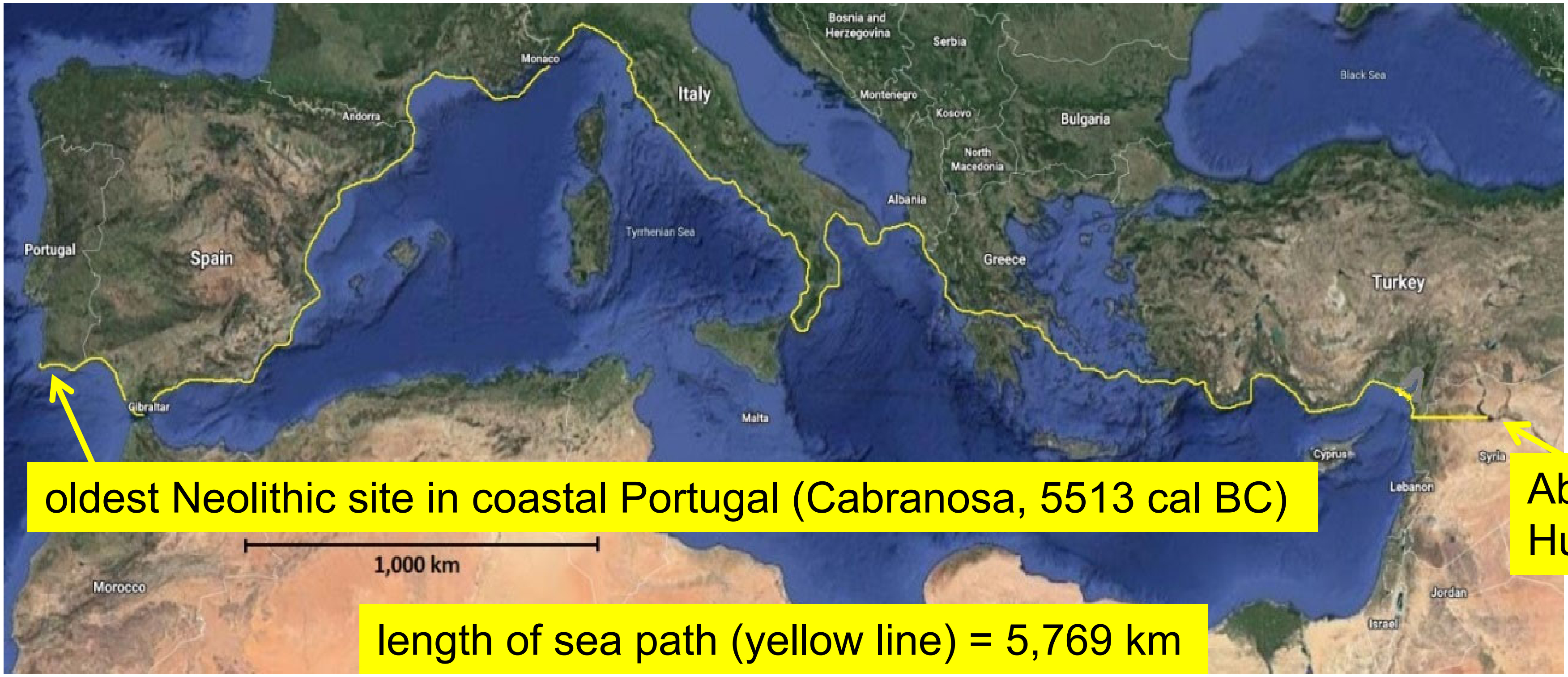


Now we have ancient genetic data for both routes

Distances

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

(2) Sea route: sea-seek.com. Example:



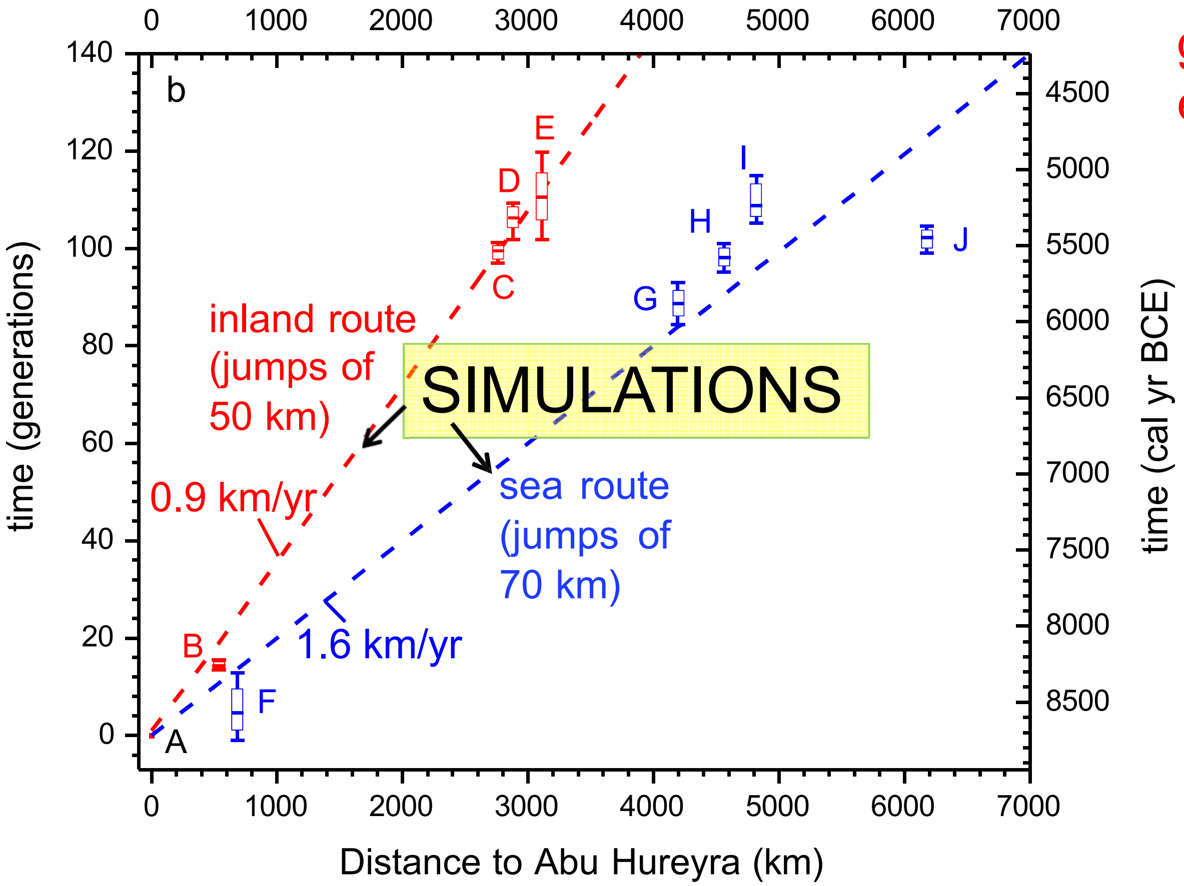
oldest Neolithic site in coastal Portugal (Cabranosa, 5513 cal BC)

Abu Hureyra

length of sea path (yellow line) = 5,769 km

Simulations + archaeological data

Initially there are farmers only at the cell with the **oldest PPNB site in Upper Mesopotamia (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.



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

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

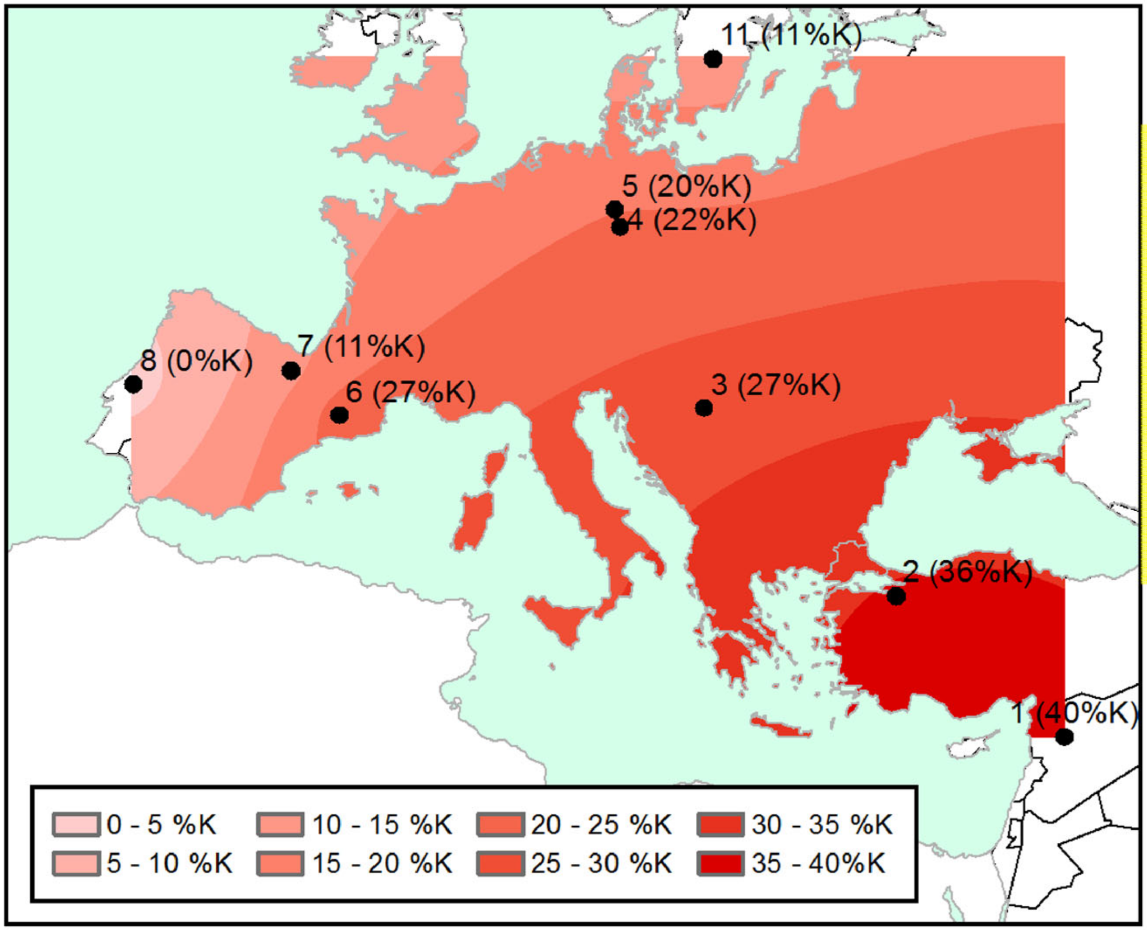
A northern Mesopotamia
B Anatolia
C Germany
D northern France
E Belgium
F Cyprus
G Southern France
H Catalonia
I Navarre
J central Portugal

LONGER JUMPS ALONG THE COAST THAN INLAND

Fort & Pérez-Losada, *Nature Comm.* 2024

Ancient genetics

mtDNA haplogroup K is the most frequent one in early farmers. It is essentially absent in HGs



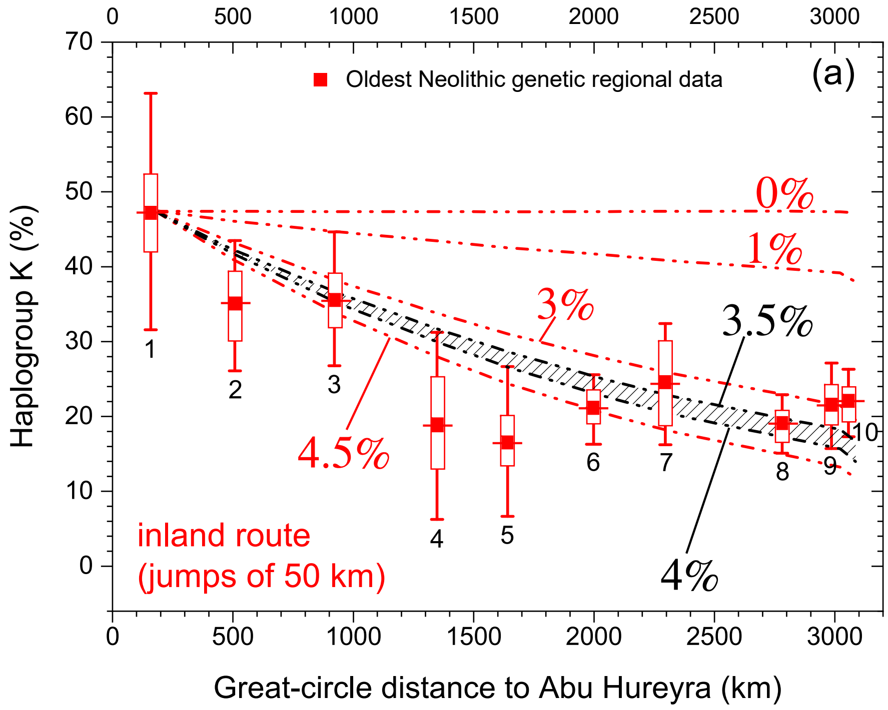
This pattern in early farmers suggests interbreeding with HGs

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

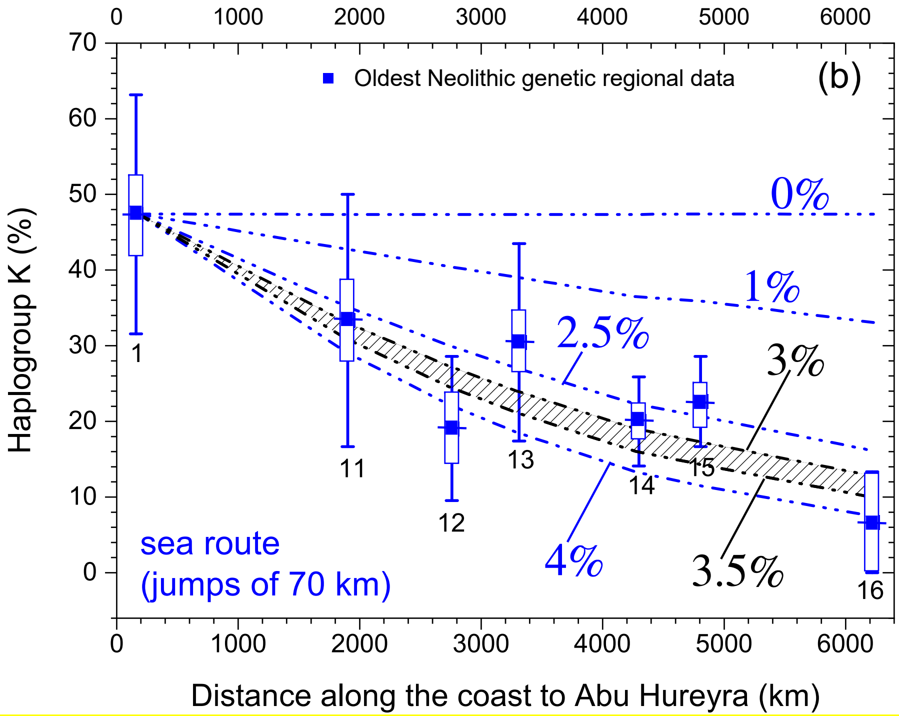
Now we have data for more regions and can analyze both routes separately

Mitochondrial haplogroup K is the most frequent one in farmers. It is essentially absent in HGs

Inland route



Sea route



Best fits: 3.5% - 4%

Best fits: 3% - 3.5%

The percentage of early farmers who interbred with HGs was essentially the same (~3.5%)!

Fort & Pérez-Losada, *Nature Comm.* (2024)

Previous slide:

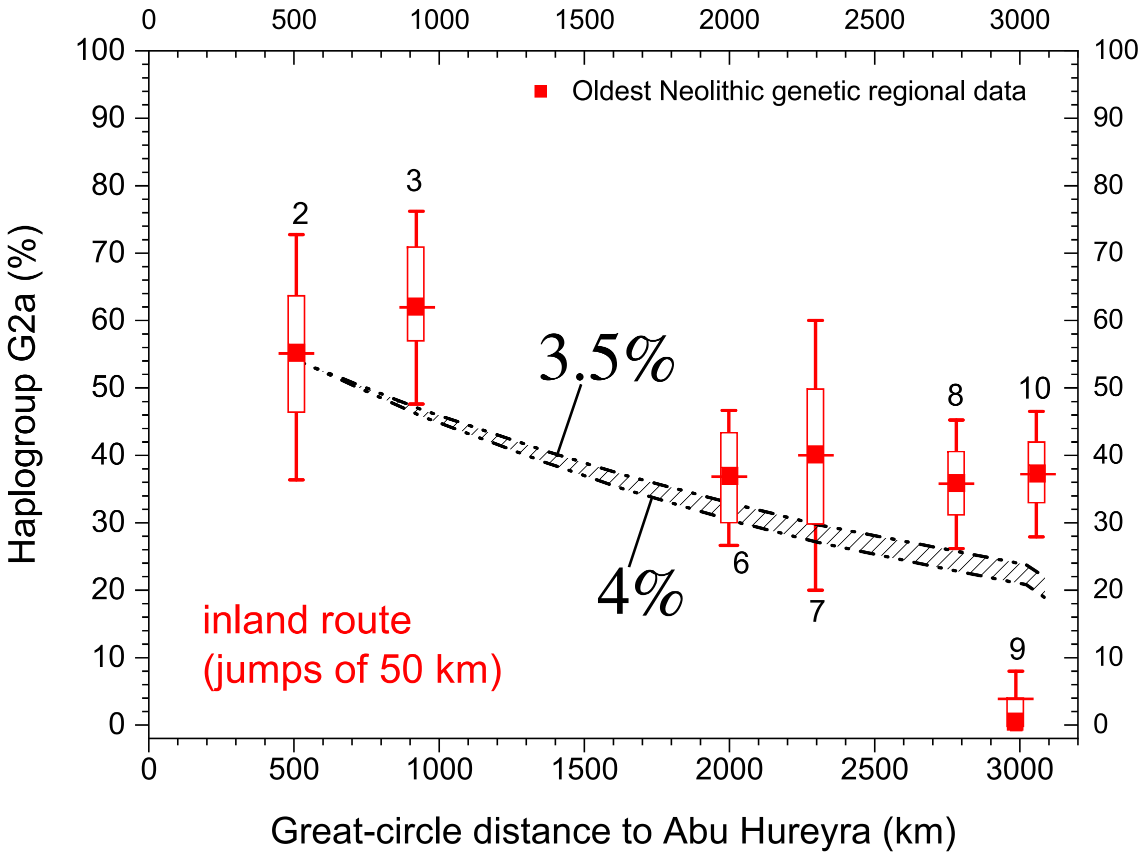
~**3.5%** of early farmers interbred with a HG

Taking into account the uncertainties in the parameter values and in the initial frequencies of haplogroup K:

1% - 8% of early farmers interbred with a HG

Y chromosome

Haplogroup G2 is the most frequent one in farmers.
It is essentially absent in hunter-gatherers

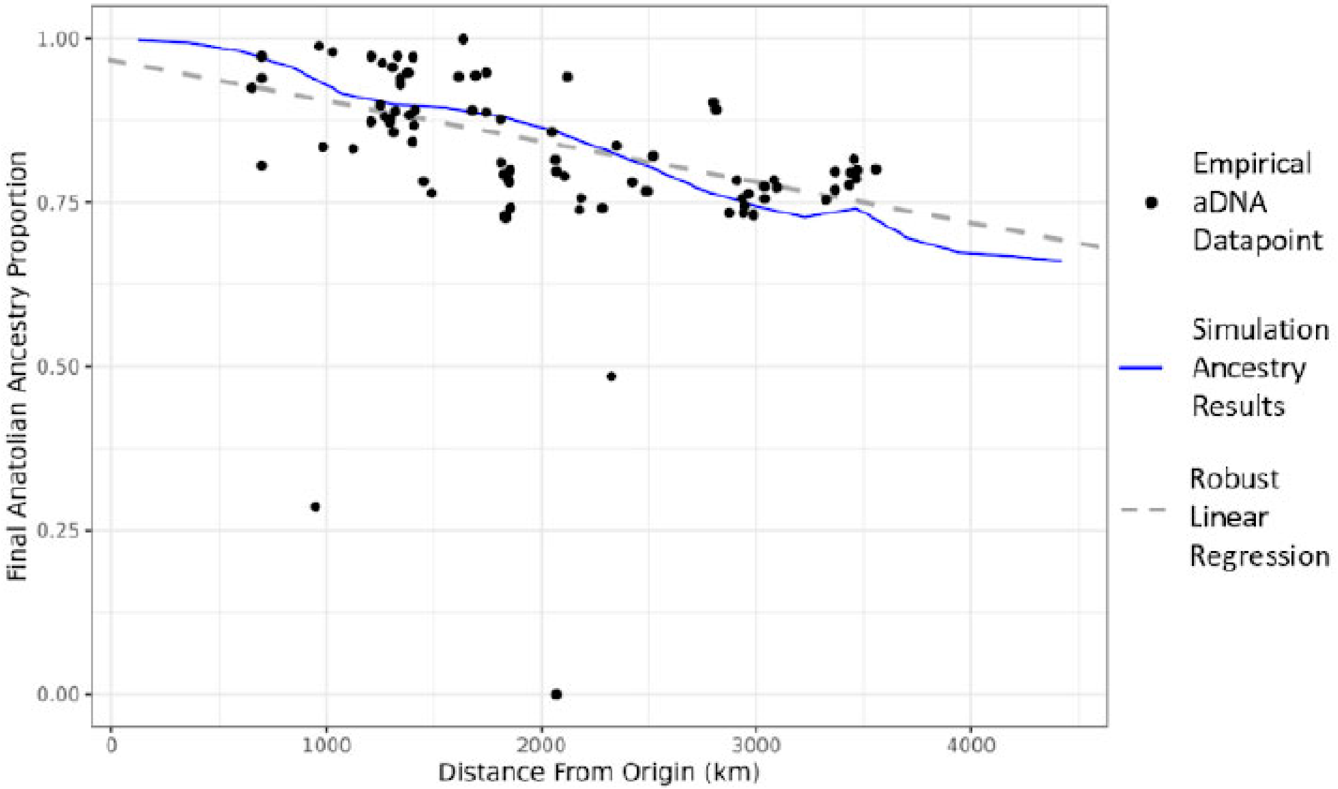


We obtain again ~**3.5%**, in agreement with the mt DNA results

For the sea route there are not enough data yet.

Fort & Pérez-Losada, *Nature Comm.* (2024)

Whole genome



LaPolice, Williams & Huber, *Nature Comm.* (2025)

Blue line assumes that 0.1% of early farmers acculturated a HG per year, i.e. about 0.1% · 32 yr = 3.2% per generation.

This is consistent with our estimation that 1% - 8% of early farmers interbred with a HG or acculturated him/her.

Conclusions

· Archaeology + SIMULATIONS tell us that: concerning dispersal, geography had a very important effect: early farmers moved longer distances per generation along the sea route than inland.

· In sharp contrast to this, ancient genetics + SIMULATIONS tell us that: the interbreeding percentage of farmers was essentially 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.

· **3 different kinds of data** (mtDNA, Y-chromosome and the whole genome) lead to the **same result**: **between 1% and 8%** of early farmers interbred with a HG or acculturated him/her.