Origins of R-M269 Diversity in Europe

Michael Hammer University of Arizona FamilyTreeDNA 9th Annual Conference

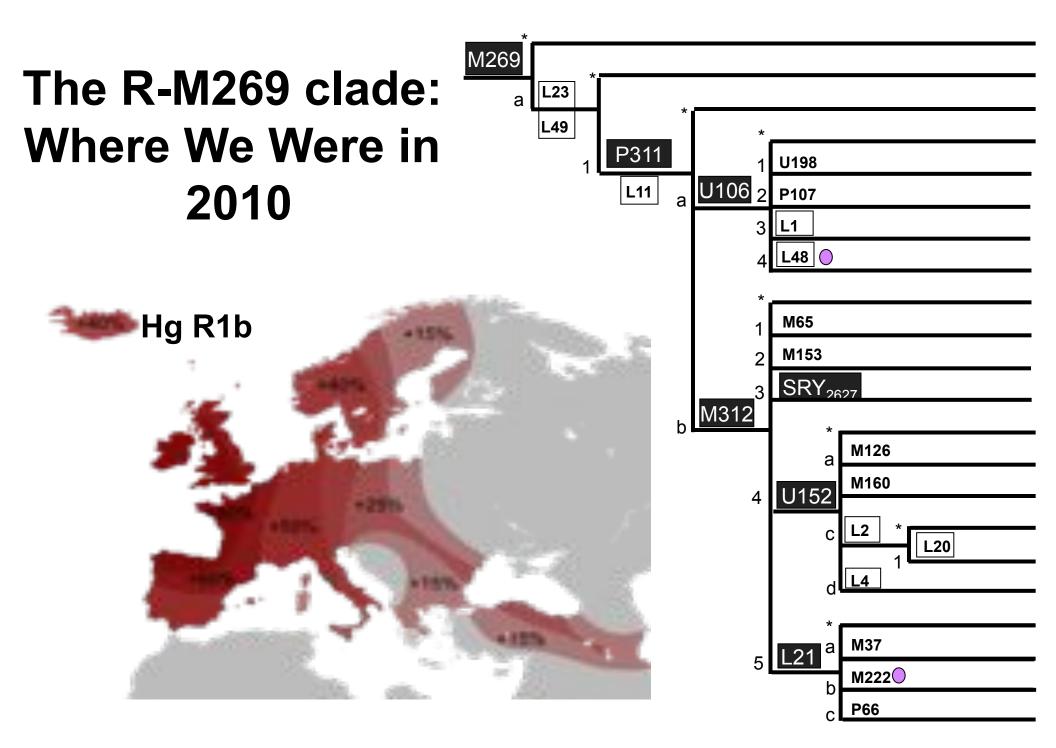
(M269)

(P297)

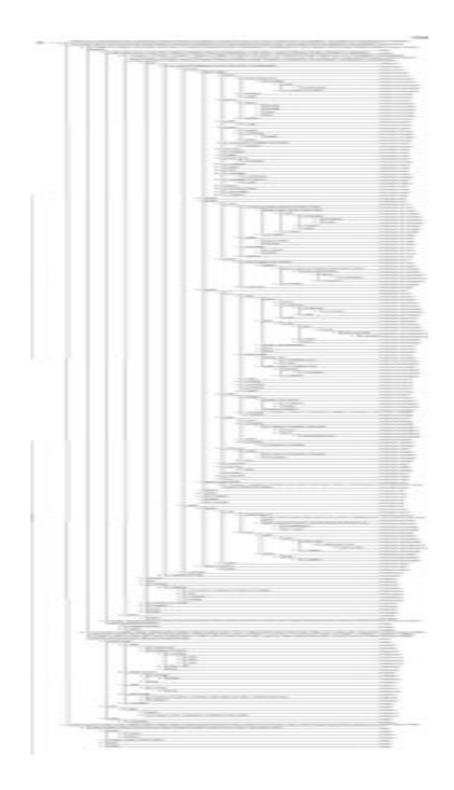
(P25)

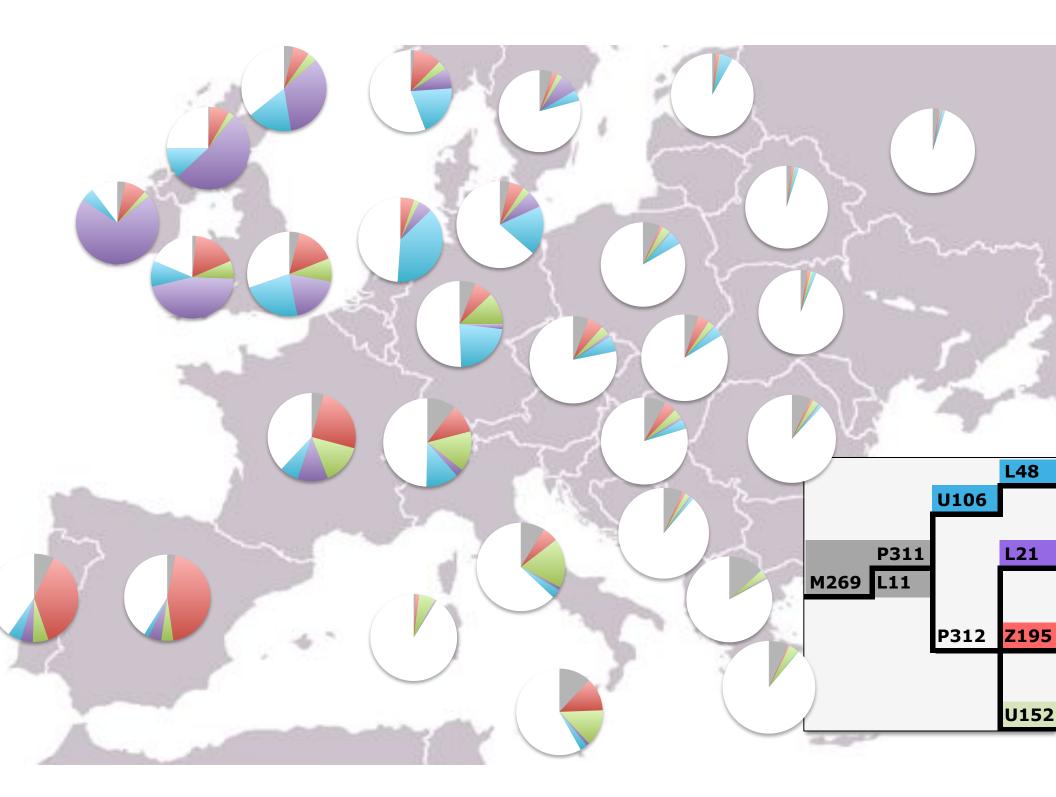
M343

72103



The R-M269 clade: Where We Are in 2013



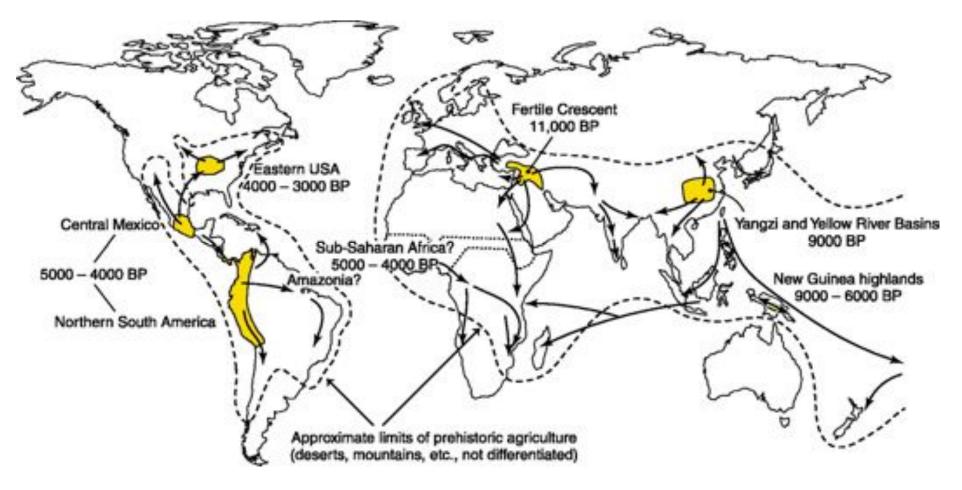


3 Major Expansions into Europe

- First anatomically modern humans (AMH) from Africa ~45,000 years ago
- After Last Glacial Maximum out of southern refugia ~17,000 years ago (Paleolithic hunter-gatherers)
- Neolithic Farmers from the Near East beginning ~10,000 years ago

Neolithic: Genes Farmers Replaced Those of Hunter-Gatherers (Diamond & Bellwood 2003)

- 9 homelands of agriculture and herding (10.5 4.5 kya)
- Food Production confers enormous advantage to farmers vs hunter-gatherers
- Triggered outward dispersals of farming populations



Europe: The Controversy

The relative contributions to modern European populations of Paleolithic hunter-gatherers and Neolithic farmers from the Near East have been intensely debated.

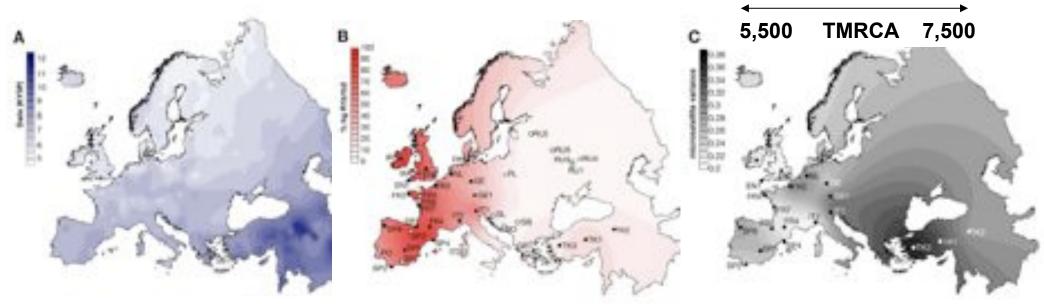
Haplogroup R-M269 is the most common European Ychromosomal lineage, increasing in frequency from east to west, and carried by 110 million European men.

Previous studies suggested a Paleolithic origin; however, two recent studies agree that this haplogroup has a more recent origin in Europe—yet they disagree on the timing of its spread.

Haplogroup R-M269 Expanded with Farming

Balaresque et al. (2010)

- Argued that geographical distribution of STR diversity on the background of R-M269 is best explained by spread from a single source in the Near East via Anatolia during the Neolithic.
- Concluded that Y chromosomes of Mesolithic hunter-gatherers were nearly replaced by those of incoming farmers, highlighting Europe as a prime example of link between technological/cultural change and expansion of a Y-chromosomal lineage.



Dates of early Neolithic sites

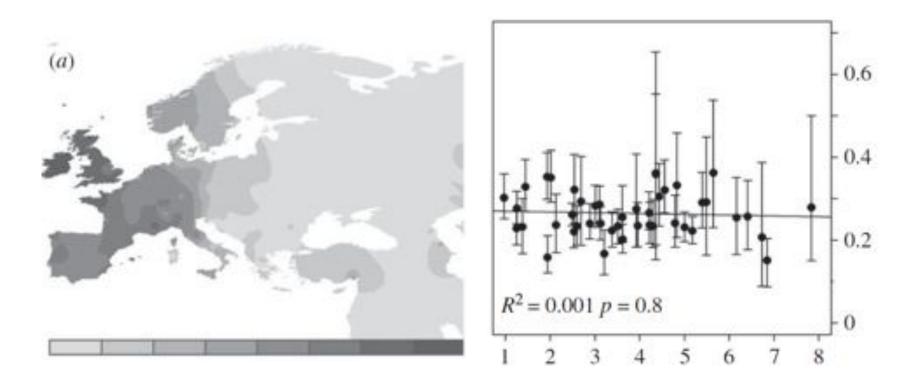
Frequency of Hg R-M269

STR diversity within Hg R-M269

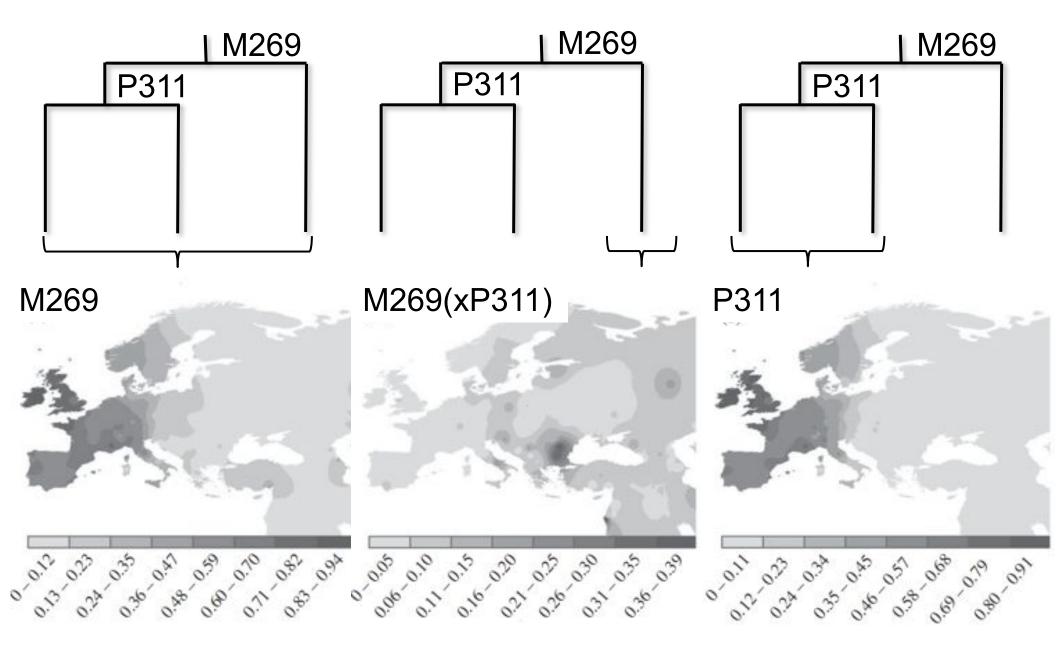
A Cautionary Tale of Y Chromosome Lineage R-M269

Busby et al. (2012)

- Performed largest study of R1b chromosomes and associated STR diversity to date (N=6,503)
- Contrary to the results of Balaresque, they saw no relationship between diversity and longitude for R-M269—a central tenet to hypothesis that R-M269 spread with expanding Neolithic farmers.
- Could not make credible estimates of the STR-based TMRCA of R-M269



Near Eastern Origin, European Expansion of R Lineages



Alternate Hypotheses: Timing of Hg R Expansion in Europe

R-P311 originated prior to the Neolithic wave of expansion and was spread during the expansion

Predicts higher diversity in the east closer to the origins of agriculture (*not observed*).

R-P311 originated more recently and its current distribution is result of major population movements *after* the Neolithic expansion.

1 Cave 1 of Treilles at St-Jean et St Paul (Aveyron, France) 5kya (end of Neolithic)

2 Abellaner Cave(Catalonia, Spain)5kya (Epicardial Culture; end of Neolithic)

3 Derenburg Cave (Meerenstieg Germany) 7kya (LBK)

4 Ötzi 5.3 kya





N=1

N=6

N=22



Latitude, Longitude	Ν	R1b (%)
1. 43.83, 5.43	38	60.5
2. 45.78, 3.08	89	52.8
3. 43.30, 5.38	45	53.3

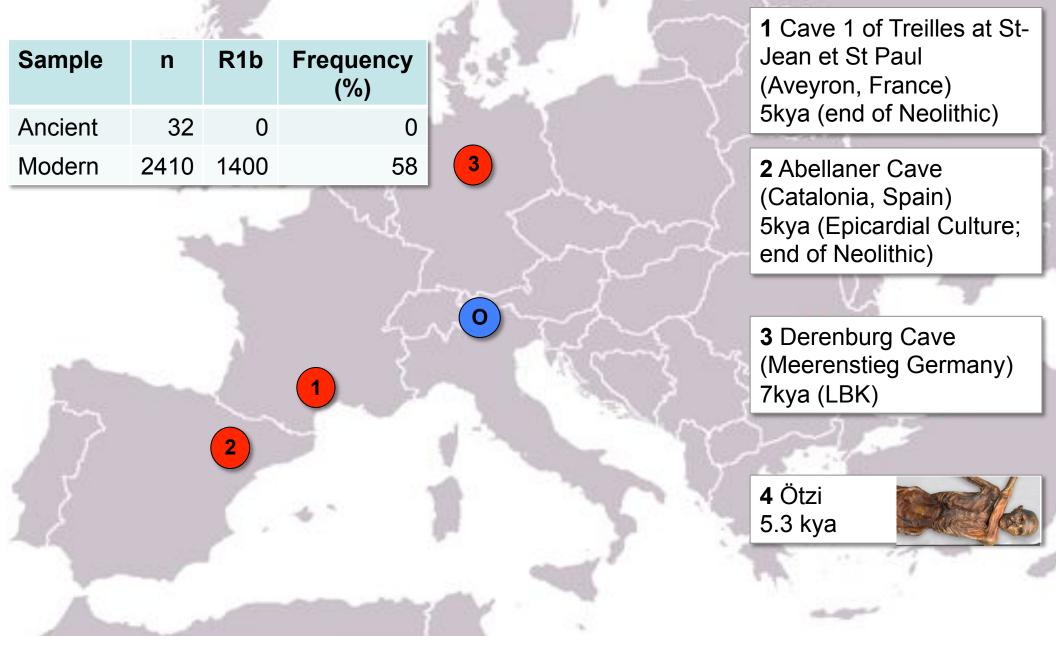
(2)

3

1 Cave 1 of Treilles at St-Jean et St Paul (Aveyron, France) 5kya (end of Neolithic)

0	R1b	other	total
Modern	94	78	172
Ancient	0	22	22

Frequency difference is highly statistically significant



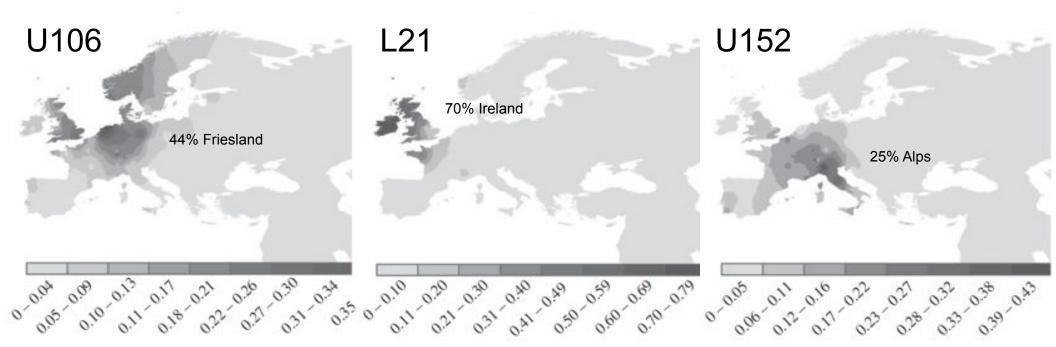
Evidence Supports a Recent Spread of Hg R Lineages in Europe

Combined evidence supports hypothesis that the current distribution of the R-P311 lineage is the result of major population movements occurring *after* the Neolithic agricultural transition.

Populations carrying R-P311 chromosomes appear to have nearly displaced western European Neolithic Y chromosomes.

What conferred advantage to post-Neolithic men?

Localized Distributions of R-U106, R-L21, and R-U152



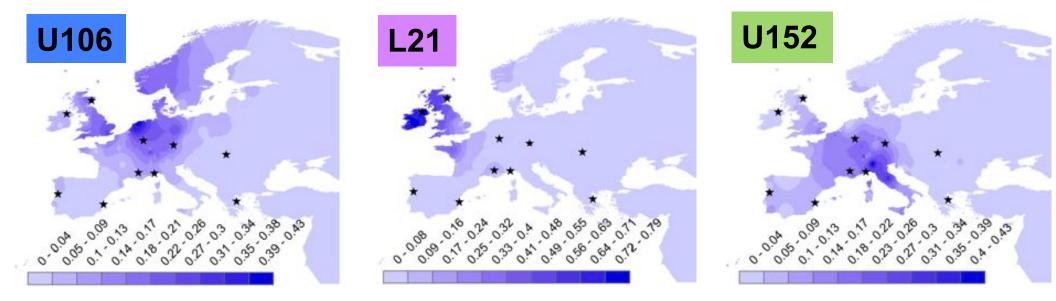
Radial distributions with epicenters in specific locations: 60% of R in C. Europe is U106-derived, 50% of R in southern Europe is U152-derived, and 45% of R in Great Britain is L21-derived

Pattern suggests differentiation across Europe via multiple geographic centers of expansion.

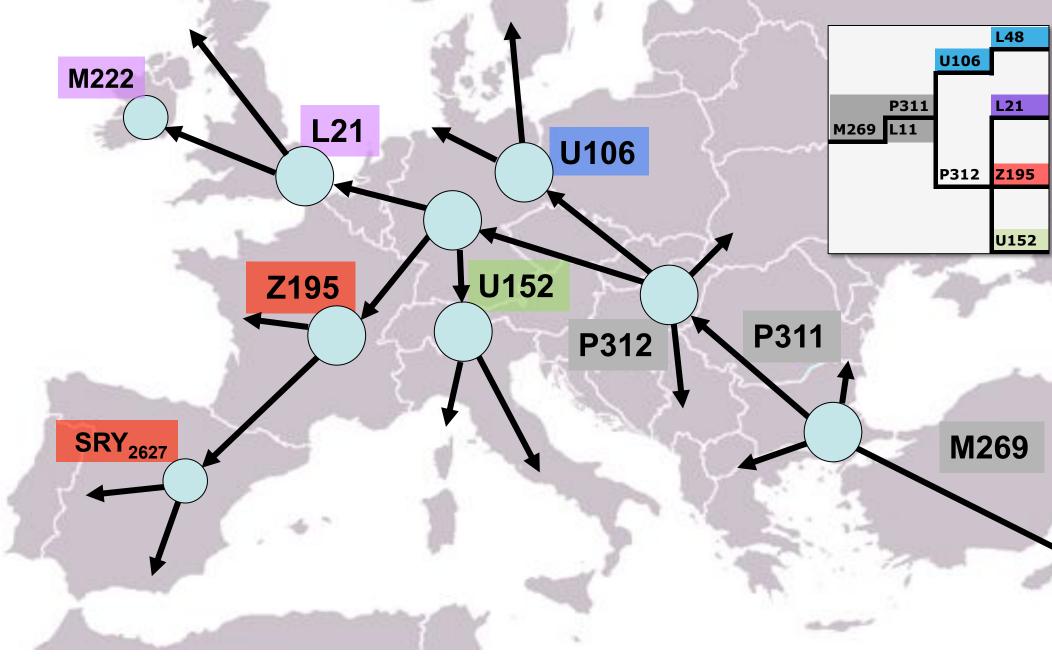
Post-Neolithic Centers of Renewed Expansion Hypothesis

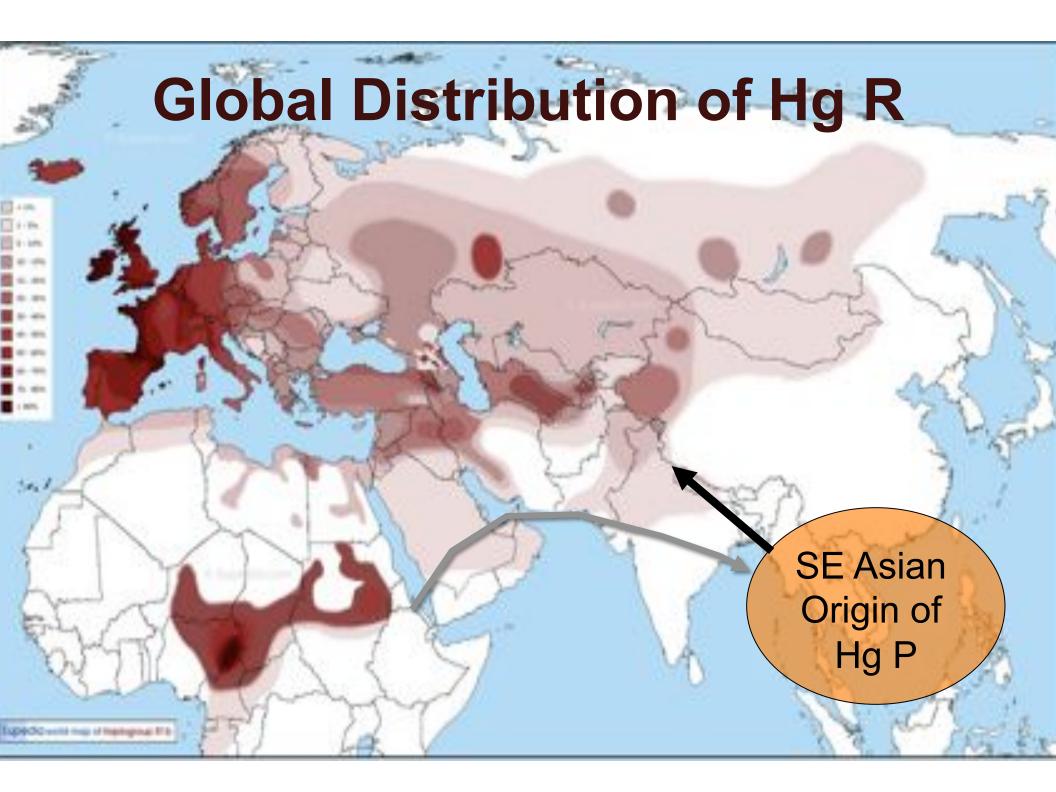
Archeological analysis of Neolithic sites across Europe reveals that the spread of the Neolithic was not constant.

Several 'centers of renewed expansion' are visible across Europe, representing areas of colonization, three of which map closely to the centers of sub-haplogroup foci.



Post-Neolithic Centers of Renewed Expansion







Early-Mid Bronze Age (4500-4000 ya)

Corded Ware Cut

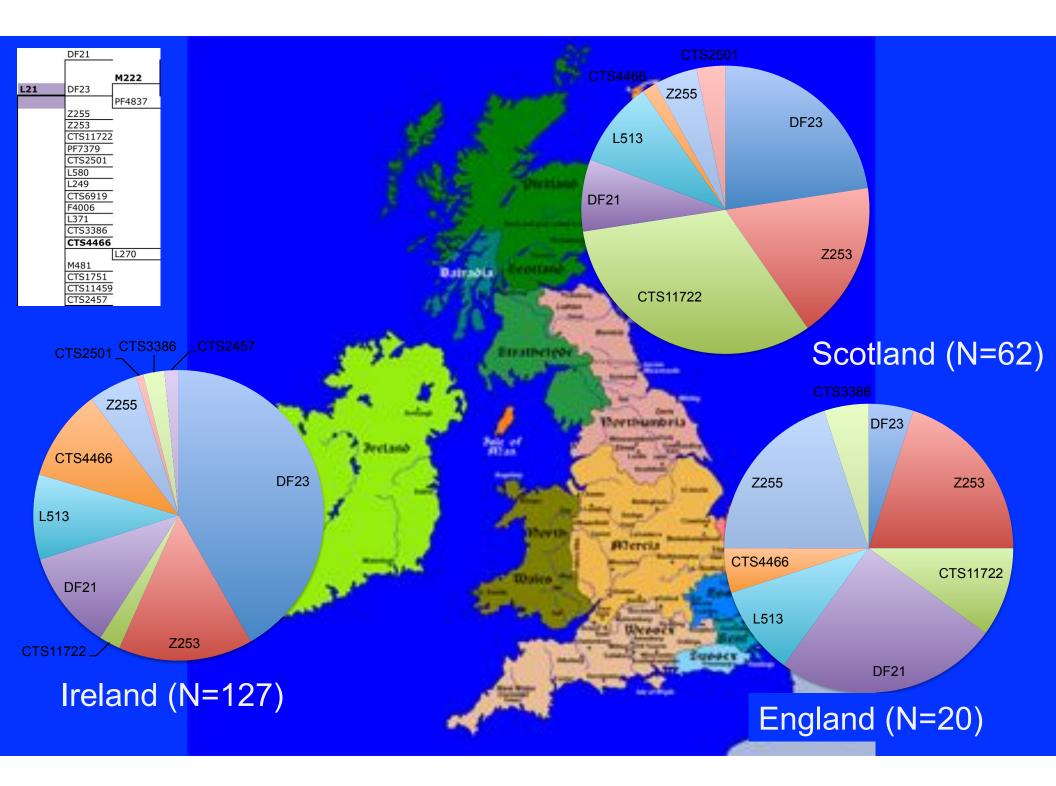
Major Metal Age Expansions

1.0.0

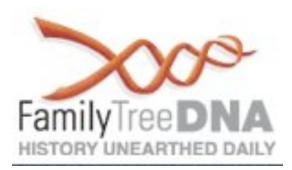
Late Bronze/Early Iron Age (3200-3000 ya)

Alteret











Tanya Karafet



Fernando Mendez



Nick Lerman Bennett Greenspan



Elliott Greenspan