R1b and the peopling of Europe: An ancient DNA update

Dr M Hammer slide presentation Family Tree DNA 11th Annual Conference Houston USA November 13th - 15th 2015

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Importance of Ancient DNA in Reconstructing Population History

- Indirect approach
 - Examine patterns of genetic variation in extant humans and infer past
- Direct approach
 - Recover DNA sequences from ancient material and compare across different time frames

Allows assessment of whether contemporary people descend from long-term inhabitants of that region, or from people who arrived from elsewhere replacing or admixing with previous inhabitants



1.

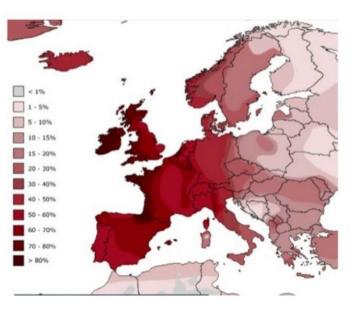
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• Direct approach – Recover DNA sequences from ancient material and compare across different time frames Allows assessment of whether contemporary people descend from long-term inhabitants of that region, or from people who arrived from elsewhere— replacing or admixing with previous inhabitants Importance of Ancient DNA in Reconstructing Population History

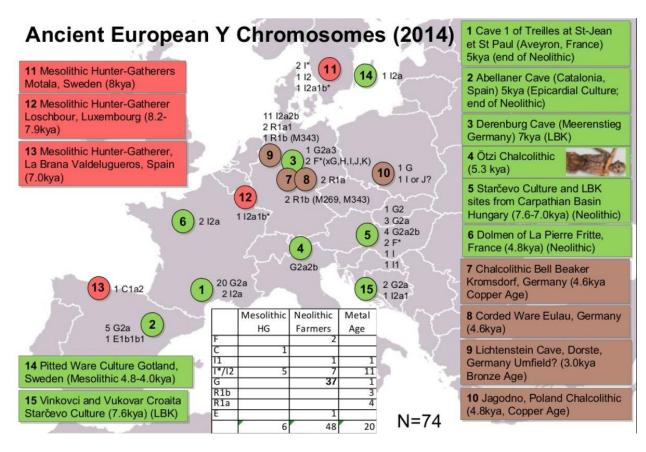
The R1b Controversy (2013)

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

2013 Conference: discussed two studies that agreed origin in Europe was **post-Paleolithic**, but differed on whether it entered Europe with Neolithic farmers or more recently.



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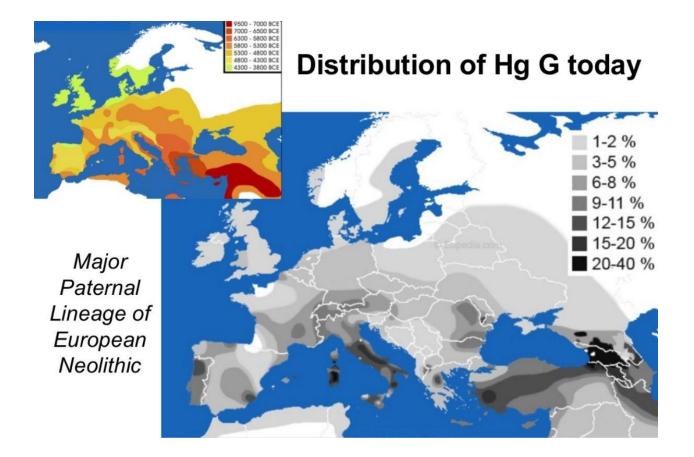


3. (references)

1 2 3 5 6 7 2 I* 1 I2 1 I2a1b* 8 9 11 I2a2b 2 R1a1 1 R1b (M343) 10 1111 Mesolithic Hunter-Gatherers Motala, Sweden (8kya) 11 Mesolithic Hunter-Gatherers Motala, Sweden (8kya) 4 12 Mesolithic Hunter-Gatherer Loschbour, Luxembourg (8.2-7.9kya) 12 Mesolithic Hunter-Gatherer Loschbour, Luxembourg (8.2-7.9kya) 12 13 Mesolithic Hunter-Gatherer, La Brana Valdelugueros, Spain (7.0kya) 13 Mesolithic Hunter-Gatherer, La Brana Valdelugueros, Spain (7.0kya) 13 14 14 Pitted Ware Culture Gotland, Sweden (Mesolithic 4.8-4.0kya) 14 Pitted Ware Culture Gotland, Sweden (Mesolithic 4.8-4.0kya) 15 Vinkovci and Vukovar Croaita Starcevo Culture (7.6kya) (LBK)? 15 Vinkovci and Vukovar Croaita Starcevo Culture (7.6kya) (LBK)? 15 20 G2a 2 I2a 5 G2a 1 E1b1b1 1 G2a3 2 F*(xG,H,I,J,K) G2a2b 2 I2a 1 C1a2 1 G 1 I or J? 2 R1b (M269, M343) 2 R1a 1 I2a1b* 1 I2a 1 G2 3 G2a 4 G2a2b 2 F* 1 I 1 I 1 2 G2a 1 I2a1 1 Cave 1 of Treilles at St-Jean et St Paul (Aveyron, France) 5kya (end of Neolithic) 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) 2 Abellaner Cave (Catalonia, Spain) 5kya (Epicardial Culture; end of Neolithic) 3 Derenburg Cave (Meerenstieg Germany) 7kya (LBK) 3 Derenburg Cave (Meerenstieg Germany) 7kya (LBK) 4 Ötzi Chalcolithic (5.3 kya) 4 Ötzi Chalcolithic (5.3 kya) 5 Starcevo Culture and LBK? sites from Carpathian Basin Hungary (7.6-7.0kya) (Neolithic) 5 Starcevo Culture and LBK? sites from Carpathian Basin Hungary (7.6-7.0kya) (Neolithic) 7 Chalcolithic Bell Beaker Kromsdorf, Germany (4.6kya Copper Age) 7 Chalcolithic Bell Beaker Kromsdorf, Germany (4.6kya Copper Age) 6 Dolmen of La Pierre Fritte, France (4.8kya) (Neolithic) 6 Dolmen of La Pierre Fritte, France (4.8kya) (Neolithic) 8 Corded Ware Eulau, Germany (4.6kya) 8 Corded Ware Eulau, Germany (4.6kya) 9 Lichtenstein Cave, Dorste, Germany Urnfield? (3.0kya Bronze Age) 9 Lichtenstein Cave, Dorste, Germany Urnfield? (3.0kya Bronze Age) 10 Jagodno, Poland Chalcolithic (4.8kya, Copper Age) 10 Jagodno, Poland Chalcolithic (4.8kya, Copper Age) Mesolithic HG Neolithic Farmers Metal Age F 2 C 1 I1 1 1 I*/I2 5 7 11 G 37 1 R1b 3 R1a 4 E 1 6 48 20 Ancient European Y Chromosomes (2014) N=74

5 of 53

2015 Presentation slides by Dr M Hammer. Reformatted by DS Marker (admin DF100-CTS4528 Project)



4. Distribution of Hg G today Major Paternal Lineage of European Neolithic

aDNA Supports a Recent Spread of Hg R Lineages in Europe

2014 Conference: Combined evidence supports hypothesis that the current distribution of Hg R lineages in western Europe is the result of major population movements occurring **after** the Neolithic agricultural transition—during the Metal Ages.

Populations carrying R1b chromosomes appear to have nearly displaced western European Neolithic Y chromosomes (Different pattern for mtDNA)

What conferred advantage to post-Neolithic men?

5. 2014 Conference: Combined evidence supports hypothesis that the current distribution of Hg R lineages in western Europe is the result of major population movements occurring after the Neolithic agricultural transition—during the Metal Ages. Populations carrying R1b chromosomes appear to have nearly displaced western European Neolithic Y chromosomes (Different pattern for mtDNA) What conferred advantage to post-Neolithic men? aDNA Supports a Recent Spread of Hg R Lineages in Europe

Post-Neolithic Turnover of W. European Y Chromosomes: Metal Weapons? (2014)

	Stone Age (Neolithic)					Bronze Age Iron Age						
Lauran haran a haran da mana haran a haran a haran da mana da m												
-9300	-8300	-7300	-6300	-5300	-4300	-3300	-2300	-1300	-30.0	700	1700	

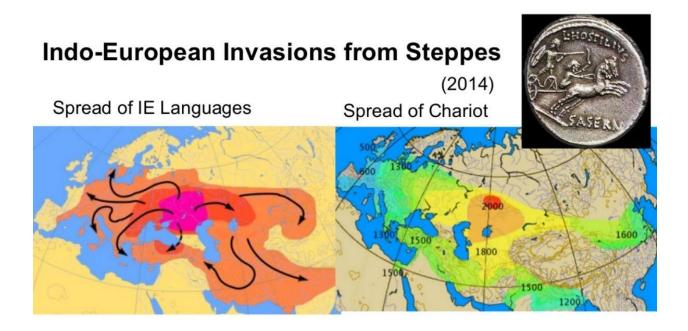
The Bronze Age: first use of metal specifically to create weapons. The sword, spear and shield were all invented in this period (warrior identity became a standard part of daily life)

The Iron Age: First true mass-production of metal tools and weapons. Revolutionizes both agriculture and



warfare. 1200 to 1000 BCE: Celts most dominant iron-age warriors. Ranging over Europe, from the British Isles to Hungary, the Celts forged tough swords made of iron.

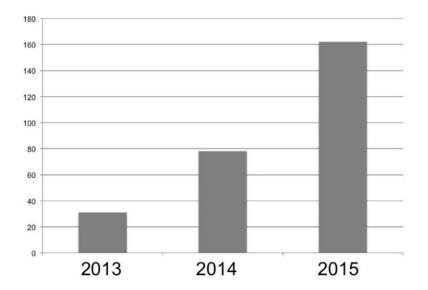
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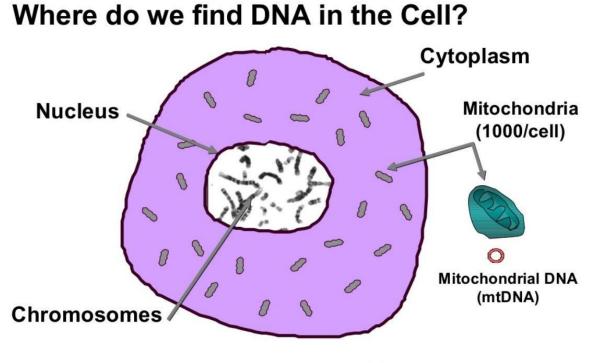
How well do our inferences from 2013 and 2014 at this conference, hold up in 2015?

7. Indo-European Invasions from Steppes How well do our inferences from 2013 and 2014 at this conference, hold up in 2015? Spread of IE Languages Spread of Chariot (2014)

Number of Ancient YDNA Samples



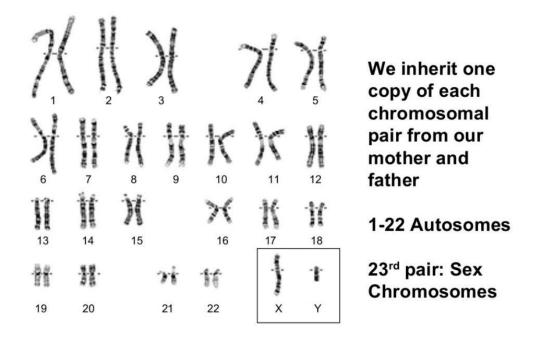
8. 2013 2014 2015 Number of Ancient YDNA Samples



Genome: the total amount of DNA in a typical cell

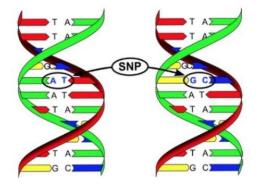
9. Mitochondria (1000/cell) Where do we find DNA in the Cell? Nucleus Chromosomes Mitochondrial DNA (mtDNA) Cytoplasm Genome: the total amount of DNA in a typical cell

Nuclear DNA: 6 Billion Nucleotides/46 chromosomes



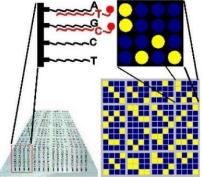
10. 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y We inherit one copy of each chromosomal pair from our mother and father 1-22 Autosomes 23rd pair: Sex Chromosomes Nuclear DNA: 6 Billion Nucleotides/46 chromosomes

Single Nucleotide Polymorphism (SNP)



A single nucleotide polymorphism (SNP)– an alteration at a single site in the DNA– is the most frequent type of variation in the genome. Currently, there are ~85 million SNPs that have been identified in the human genome.

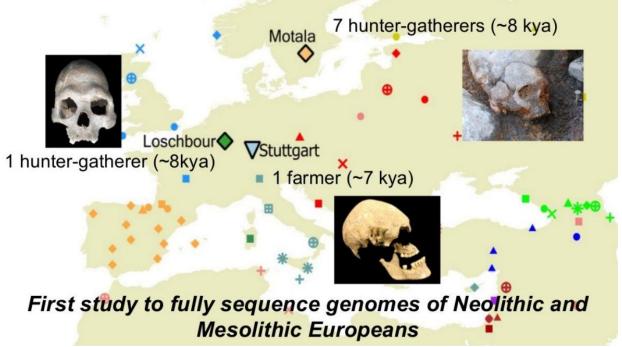
DNA microarray technology (SNP array) is used to detect SNPs within a population. SNP arrays are able to detect millions of different SNPs on all chromosomes in hundreds of samples in a single experiment.



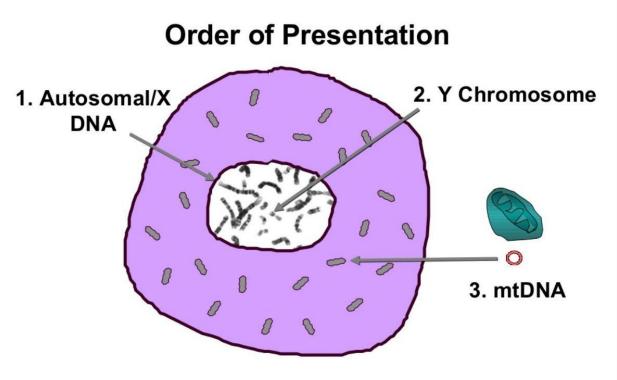
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Complete Genomes from Nine Ancient Europeans

Lazaridis et al. Nature (2014)

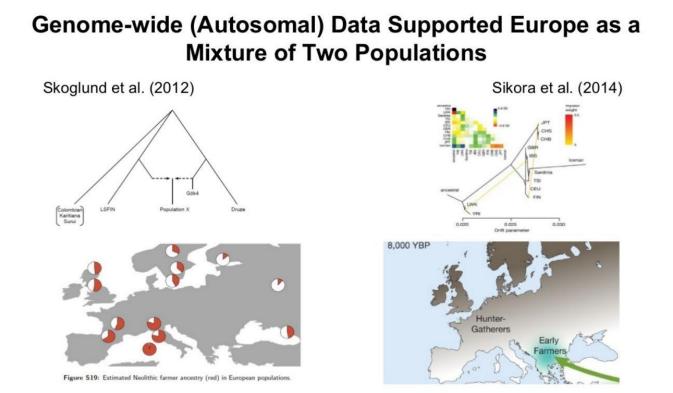


12. 1 hunter-gatherer (~8kya) 7 hunter-gatherers (~8 kya) 1 farmer (~7 kya) Complete Genomes from Nine Ancient Europeans Lazaridis et al. Nature (2014) First study to fully sequence genomes of Neolithic and Mesolithic Europeans



First: Results from Contemporary Samples, then ancient DNA

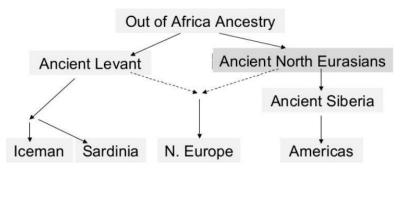
- 13. Order of Presentation
- 1. Autosomal/X DNA
- 2. Y Chromosome
- 3. mtDNA First: Results from Contemporary Samples, then ancient DNA



14. Genome-wide (Autosomal) Data Supported Europe as a Mixture of Two Populations Skoglund et al. (2012) Sikora et al. (2014)

Genes from a third source?

Patterson et al. (2012)



"The ghost population of North Eurasia"

- Genotyped >600K SNPs in >900 individuals from 53 diverse populations
- Performed admixture tests and inferred proportions and dates of mixture
- Found signal of Northeast Asian-related admixture in northern Europeans

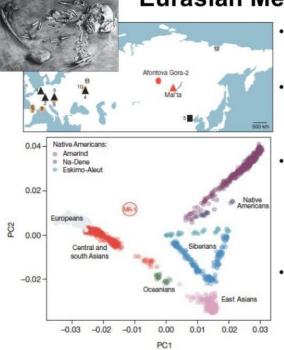
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The Ghost is Identified: Discovery of Ancient North Eurasian Meta-Population Rahavan et al. (2013)



- Sequenced genome of ~24,000 year old Siberian individual (Mal'ta or MA1)
- MA1 is genetically similar to Native Americans and West Eurasians (not close to East Asians)
- Sequencing of another south-central Siberian (Afontova Gora-2) dating to ~17 kya revealed similar genetic signatures, suggesting the persistence of an ancient North Eurasian meta-population (**ANE**)
- What is the relationship of ANE to ancient H-G and farming populations that contributed ancestry to contemporary Europeans?

16. The Ghost is Identified: Discovery of Ancient North Eurasian Meta-Population Raghavan et al. (2013) • Sequenced genome of ~24,000 year old Siberian individual (Mal'ta or MA1) • MA1 is genetically similar to Native Americans and West Eurasians (not close to East Asians) • Sequencing of another south-central Siberian (Afontova Gora-2) dating to ~17 kya revealed similar genetic signatures, suggesting the persistence of an ancient North Eurasian meta-population (ANE) • What is the relationship of ANE to ancient H-G and farming populations that contributed ancestry to contemporary Europeans? Rahavan et al. (2013)

European Ancestral Components: Rooted in Ancient DNA

- West European Hunter-Gatherer (**WHG**), based on an 8,000 year-old genome from Loschbour, Luxembourg. The WHG meta-population includes the Swedish hunter-gatherers and a Mesolithic individual from the La Brana Cave in Spain.
- Early European Farmer (EEF), based on a 7,500 year-old genome from Stuttgart, Germany, belonging to the Neolithic Linearbandkeramik (LBK) culture. The EEF meta-population includes Oetzi the Iceman and a Neolithic Funnelbeaker farmer from Sweden.
- Ancient North Eurasian (ANE), based on the 24,000 year-old genome from Mal'ta Siberia. The ANE meta-population includes Mal'ta (MA1) boy as well as the late Upper Paleolithic sample from Central Siberia called Afontova Gora-2 (AG2).

17.

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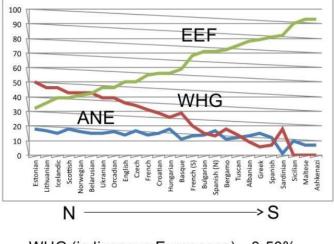
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Geographic Variation in European Ancestral Components



WHG (indigenous Europeans)0-50%EEF (Near Eastern origin)32-93%ANE (like ancient Siberians)1-18%

First Farmers only a mixture of 2 source populations

- EEF component increases towards the South, peaking at just over 80% among Sardinians
- In contrast, WHG component increases towards the North, peaking in the East Baltic region at ~50%.No detectable WHG ancestry in the Near East
- ANE ancestry is present in nearly all Europeans today at lower levels, peaking in Estonians & Scots at just over 18% (absent in Sardinians)
- Importantly, ANE component is not found in either farmers or HGs from central and western Europe during the Neolithic

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Three Source Migration Model for Europe

- European Hunter-Gatherers
- Early European Farmers
- Ancient North Eurasians

Anatomically modern hunter-gatherers first migrated into Europe ~45 kya from Africa through the Levant

Second major infusion of people comes with expansion of agriculture—also from the Levant—beginning ~8 kya After 7,000 years ago

ANE ancestry component entered the broader European gene pool after the Neolithic

S. Europeans inherited their hunter-gatherer ancestry mostly via EEF ancestors, whereas N. Europeans retain up to 50% of WHG ancestry above and beyond what they received through mixing with more recent EEF ancestors.

45,000 years ago 7,000 years ago

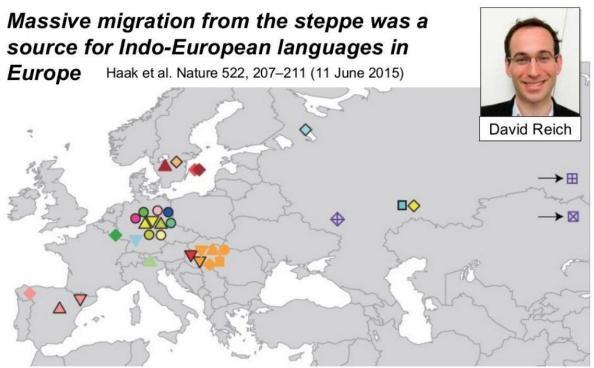
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Who were the ANE and how did they make such a large contribution to the European Gene Pool?

- · Turns out that the spread of R1b into Europe can be traced to the ANE
- Can we associate the initial entry of R1b into Europe with the innovation of the chariot, production of new weapons and training of horses, and the spread of the Indo-European languages in the Bronze Age (2700 BCE to 500 BCE)?
- Two laboratories published papers in the same issue of Nature this past June- both reaching the same conclusion. Massive migrations from the Russian Steppe in the Bronze Age represents the third major source of genetic material found in Europeans today
- They extracted genetic material from bones and teeth collected from across Europe and as far east as Lake Baikal in Siberia. The age of the bones spanned five millennia, from 6,000 to 900 BCE
- To get the 170 samples, they had to test >700 samples for DNA quality. All of the samples that they ultimately used for analysis had a well-documented archaeological context with radio carbon dates

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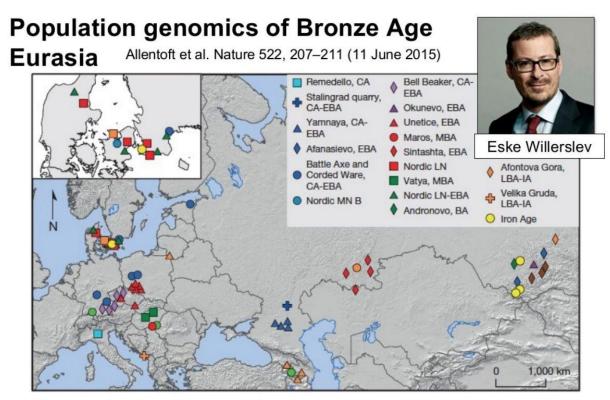
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Used novel technique to enrich ancient DNA for a set of ~400,000 SNPs and generate genome-wide data from 69 ancient Europeans

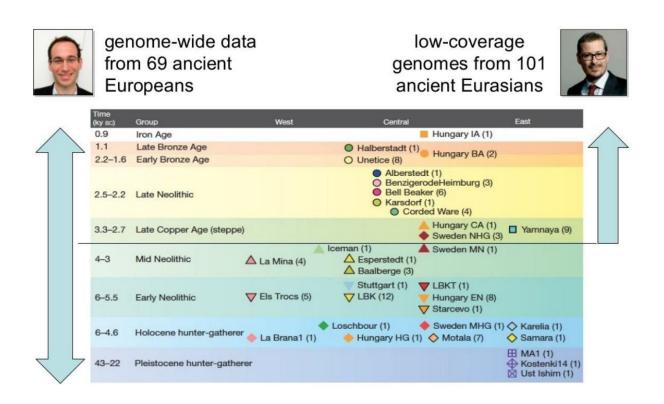
21.

Massive migration from the steppe was a source for Indo-European languages in Europe Haak et al. Nature 522, 207–211 (11 June 2015) Used novel technique to enrich ancient DNA for a set of ~400,000 SNPs and generate genome-wide data from 69 ancient Europeans David Reich

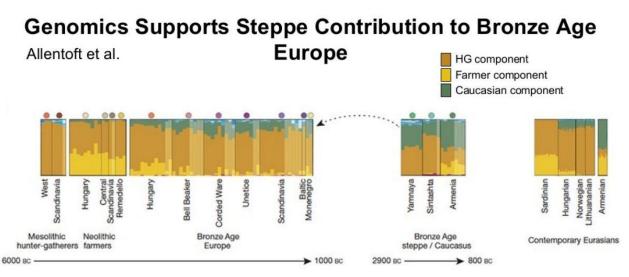


Used improved methods to generate low-coverage genomes from 101 ancient Eurasians

22. Population genomics of Bronze Age Eurasia Allentoft et al. Nature 522, 207–211 (11 June 2015) Eske Willerslev Used improved methods to generate low-coverage genomes from 101 ancient Eurasians



23. low-coverage genomes from 101 ancient Eurasians genome-wide data from 69 ancient Europeans



- Neolithic Europe populations composed of mixture of the hunter-gatherer and Neolithic farmer groups
- Bronze Age European populations have added 'Caucasian' component suggested to derive from Yamnaya culture from the Pontic-Caspian steppe
- Neolithic farmer component is absent in Yamnaya and at very low levels in present-day Norwegians and Lithuanians
- · Yamnaya component is absent in present-day Sardinians

24.

• Neolithic Europe populations composed of mixture of the hunter-gatherer and Neolithic farmer groups

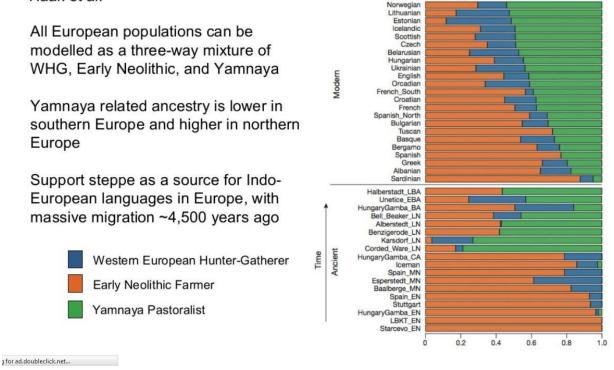
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• Yamnaya component is absent in present-day Sardinians Genomics Supports Steppe Contribution to Bronze Age Europe HG component Farmer component Caucasian component Allentoft et al.

Yamnaya genetic contribution to Neolithic European Gene Pool

Haak et al.

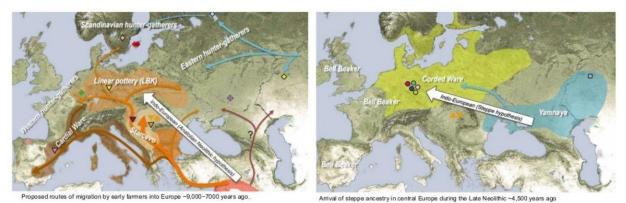


25.

All European populations can be modelled as a three-way mixture of WHG, Early Neolithic, and Yamnaya.

Yamnaya related ancestry is lower in southern Europe and higher in northern Europe Support steppe as a source for Indo- European languages in Europe, with massive migration ~4,500 years ago Yamnaya genetic contribution to Neolithic European Gene Pool Haak et al. Western European Hunter-Gatherer Early Neolithic Farmer Yamnaya Pastoralist

Allentoft & Haak Studies Agree



- Three groups of hunter-gatherers initially populated Europe: Western; Eastern, and Scandinavian HG
- Early farmers of Europe migrated into Europe ~9,000-7,000 years ago.
- Yamnaya pastoralists arrived in central Europe from the Russian steppe during the Late Neolithic ~4,500 years ago.
- The resulting Corded Ware culture in Europe was the result of admixture with the local Neolithic people.

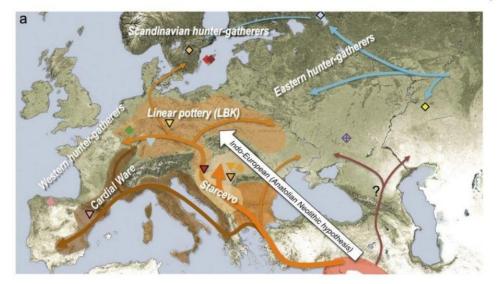
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Middle Neolithic Resurgence of HG Ancestry throughout Europe

Haak et al. (2015)

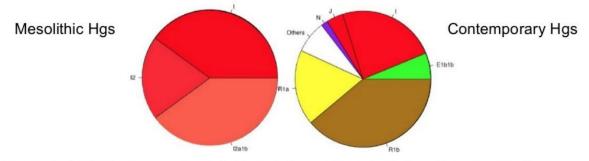


Resurgence of hunter-gatherer ancestry during the Middle Neolithic 7,000-5,000 years ago

27. Resurgence of hunter-gatherer ancestry during the Middle Neolithic 7,000-5,000 years ago Middle Neolithic Resurgence of HG Ancestry throughout Europe Haak et al. (2015)

Connecting the Dots: What does the new model of European ancestry based on autosomal DNA mean for the NRY and mtDNA?

- Which population(s) carried the most common contemporary NRY haplogroups into Europe and when?
- How does the Caucasian/Yamnaya ancestry component seen in autosomal DNA correspond to the NRY and mtDNA?



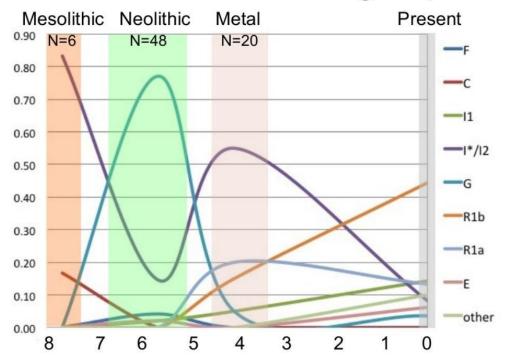
Pie chart of NRY haplogroups of individuals in Lazaridis et al. study and present day Germans. While only haplogroup I was found in Mesolithic hunter-gatherers, this haplogroup is a minority in present-day Europeans from Germany.

28. Connecting the Dots:

• What does the new model of European ancestry based on autosomal DNA mean for the NRY and mtDNA?

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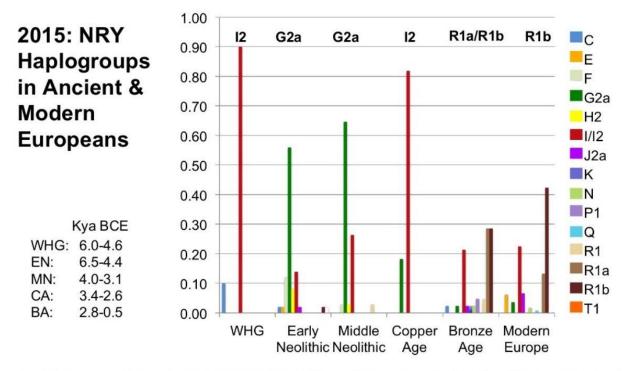
• How does the Caucasian/Yamnaya ancestry component seen in autosomal DNA correspond to the NRY and mtDNA? Pie chart of NRY haplogroups of individuals in Lazaridis et al. study and present day Germans. While only haplogroup I was found in Mesolithic hunter-gatherers, this haplogroup is a minority in present-day Europeans from Germany. Mesolithic Hgs Contemporary Hgs



2014: Ancient & Modern NRY Hg Frequencies

29. 2014: Ancient & Modern NRY Hg Frequencies N=6 N=48 N=20

Mesolithic Neolithic Metal Present Thousands of Years Ago 8 7 6 5 4 3 2 1 0



Increase in Hg I may reflect resurgence in WHG lineages in Middle Neolithic, consistent with autosomal data

30. 2015: NRY Haplogroups in Ancient & Modern Europeans

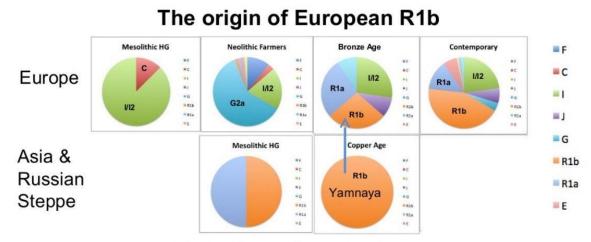
WHG: 6.0-4.6

EN: 6.5-4.4

MN: 4.0-3.1

CA: 3.4-2.6

BA: 2.8-0.5 Kya BCE I2 G2a G2a I2 R1a/R1b R1b Increase in Hg I may reflect resurgence in WHG lineages in Middle Neolithic, consistent with autosomal data



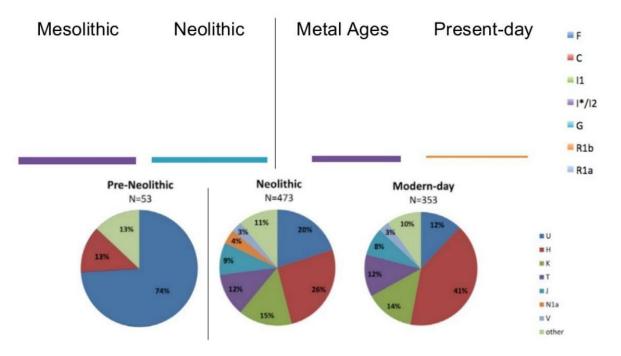
- In Europe, only a single R1b individual found before Late Neolithic
- · By contrast, R1a and R1b found in 60% of Bronze Age Europeans
- Highest frequency of R1b found in Copper Age Yamnaya of the Russian Steppe the same population that contributed the autosomal 'Caucasian' component to Bronze Age Europeans
- Combined results suggest that R1b spread into central and western Europe from the steppe after 3,000 BCE (*in agreement with our inferences here in 2013 and 2014!*)

31.

• In Europe, only a single R1b individual found before Late Neolithic

• By contrast, R1a and R1b found in 60% of Bronze Age Europeans • Highest frequency of R1b found in Copper Age Yamnaya of the Russian Steppe - the same population that contributed the autosomal 'Caucasian' component to Bronze Age Europeans

• Combined results suggest that R1b spread into central and western Europe from the steppe after 3,000 BCE (in agreement with our inferences here in 2013 and 2014!) The origin of European R1b Europe Yamnaya Asia & Russian Steppe Bronze Age R1b R1b R1a G2a I/I2 I/I2 I/I2 R1b R1a C I/I2



2014: NRY & mtDNA Discontinuities

32. 2014: NRY & mtDNA Discontinuities Mesolithic Neolithic Metal Ages Present-day

Off with their heads and onto their women!



33. Off with their heads and onto their women!

Key mtDNA Results

Haak et al.

- Hunter-gatherers carry predominantly U-haplotypes
- Early farmers predominantly carry haplotypes T2, K, HV, H, V, X and N1a
- Middle Neolithic farmers exhibit a similar mitochondrial profile as early farmers but show an increase in the frequency of Uhaplotypes (providing mitochondrial DNA based evidence of the resurgence of hunter-gatherer lineages that was documented from autosomal data)
- Late Neolithic individuals mark a second major turnover, highlighted by the appearance of I, T1, and increase of U2, U4, U5a, H and W haplotypes

34. Haak et al.Key mtDNA Results

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mtDNA haplogroup N1a and Y chromosome haplogroup G2a, common in early central European farmers, almost disappear during the Late Neolithic and Bronze Age, when they are largely replaced by Y haplogroups R1a and R1b and mtDNA haplogroups I, T1, U2, U4, U5a, W, and subtypes of H14, 23, 24.

The uniparental data not only confirm a link to the steppe populations but also suggest that both sexes participated in the migrations.



rring data from image.slidesharecdn.com...

35.

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Ratio of Bronze Age Y to ANE Contribution to Modern Europeans Varies by Location

1.83	Estonian	0.93	Belarusian	0.53	Croatian
1.59	Spanish (N)	0.87	Ukranian	0.43	Bulgarian
2.25	Spanish (S)	1.00	Lithuanian	1.08	Tuscan
1.71	French	0.93	AVE	1.15	Albanian
1.64	English			0.67	Greek
1.35	Czech			0.77	AVE
1.28	Hungarian	0.81	Norwegian		
1.06	Scottish				
1.59	AVE				

High

Male Bias

Low

36

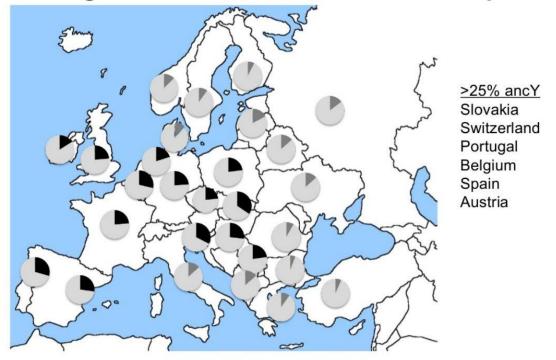
.1.83 Estonian 0.93 Belarusian 0.53 Croatian 1.59 Spanish (N) 0.87 Ukranian 0.43 Bulgarian 2.25 Spanish (S) 1.00 Lithuanian 1.08 Tuscan 1.71 French 0.93 AVE 1.15 Albanian 1.64 English 0.67 Greek 1.35 Czech 0.77 AVE 1.28 Hungarian

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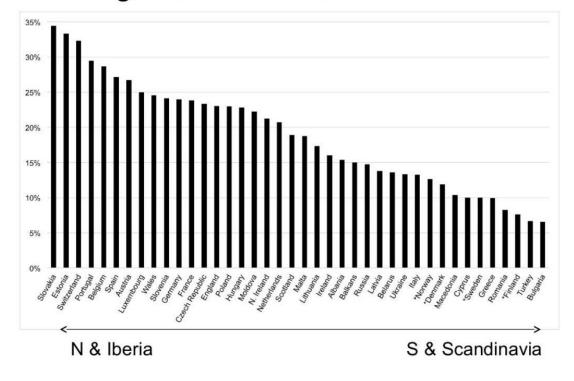
1.59 AVE Ratio of Bronze Age Y to ANE Contribution to Modern Europeans Varies by Location Male Bias High Low

Bronze Age FtDNA Y chromosomes in Europeans



37. Bronze Age FtDNA Y chromosomes in Europeans >25% ancY Slovakia Switzerland Portugal Belgium Spain Austria

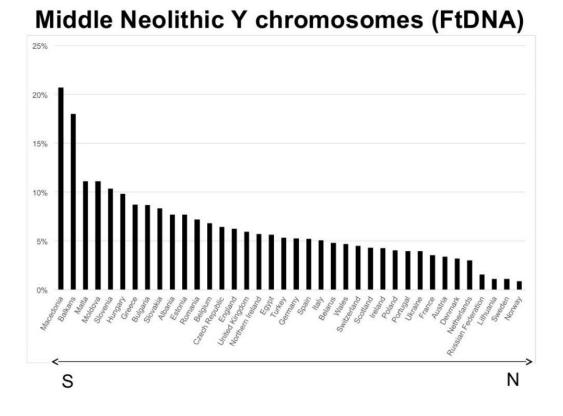
Bronze Age Y chromosomes in FtDNA Database



38. Bronze Age Y chromosomes in FtDNA Database N & Iberia S & Scandinavia

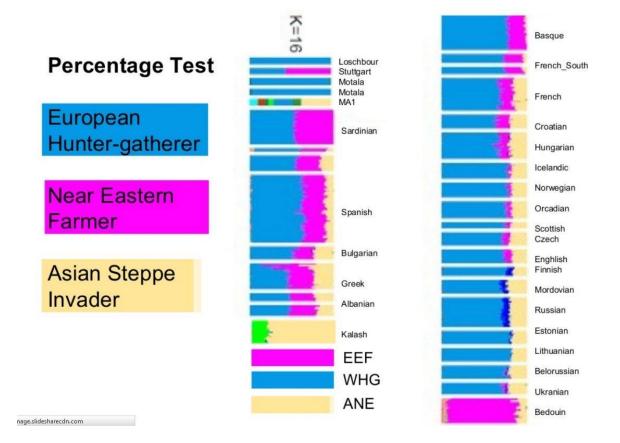
WHG Y Chromosomes in FtDNA Database

39. S N WHG Y Chromosomes in FtDNA Database



40. Middle Neolithic Y chromosomes (FtDNA) S N

41. Ancient Y Haplogroups by Cultural Periods WHG 8.0-6.6 kya Middle Neolithic 8.5-5.1 kya Bronze Age 4.8-2.5 kya P37.2 L178 M423 V20 L596 L597 M269, L265, L773, L265, L500, L482 L483, L150.1, M512, M459, M417, P310 P217, P218, L181, CTS9183, CTS616, L596, L597, L26 M17, M198, Z91, L51, U106, P312 U152, M170, L146, M420, M173, P241 P215, M343 P15 P37.2 L158 M26 PF3146 L91 L281 P96 L284 L285 L286 M170 Z161



42. ANE EEF WHG Loschbour Stuttgart Motala Motala MA1 Sardinian Spanish Bulgarian Greek Albanian Kalash Basque French_South French Croatian Hungarian Icelandic Norwegian Orcadian Scottish Czech Enghlish Finnish Mordovian Russian Estonian Lithuanian Belorussian Ukranian Bedouin Percentage Test European Hunter-gatherer Near Eastern Farmer Asian Steppe Invader

A Y Chromosome Roller Coaster

The frequency of haplogroup I, Europe's Mesolithic paternal marker, was strongly affected by incoming farmers in the early Neolithic—made a comeback in the Middle Neolithic—only to be partially replaced again during the Metal Ages.

Haplogroup G2a, Europe's Neolithic marker, had a very different fate: it's predominance in the Neolithic contrasts sharply with it's near absence in the subsequent ancient DNA record and it's limited distribution today in the southern Europe and the eastern Mediterranean

In contrast, the predominant haplogroup in western Europe today, R1b, made a late entrance– nearly absent from the ancient DNA record until the Bronze age when it swept into central Europe with the entry of Asian/Eastern European steppe invaders

While it is clear that the post-Neolithic arrival of steppe invaders across much of Europe led to major upheavals during the Early Bronze Age— this was a period that saw the introduction of metal weapons and a new social organization across most of the continent—a further assessment is needed to determine the degree to which there was a sex-bias in the replacement process

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46 of 53

2015 Presentation slides by Dr M Hammer. Reformatted by DS Marker (admin DF100-CTS4528 Project)

A cautionary tale for interpreting patterns of contemporary variation

Contemporary populations from across great parts of western, northern and central Europe show greater genetic affinities with local Bronze Age groups in the Russian steppes than with earlier Mesolithic and Neolithic groups living in Europe.

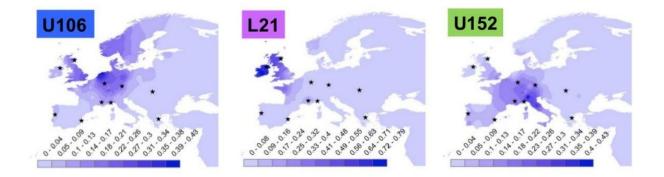
Much of the basis of the Eurasian genetic landscape of today was formed during the complex patterns of expansions, admixture and replacements during a relatively short period of time

Subsequent increases in population size combined with continuing gene flow between populations led to diffusion of genetic material generating much lower differentiation among contemporary populations compared with the Bronze Age.

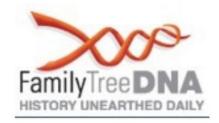
44. Contemporary populations from across great parts of western, northern and central Europe show greater genetic affinities with local Bronze Age groups in the Russian steppes than with earlier Mesolithic and Neolithic groups living in Europe. Much of the basis of the Eurasian genetic landscape of today was formed during the complex patterns of expansions, admixture and replacements during a relatively short period of time Subsequent increases in population size combined with continuing gene flow between populations led to diffusion of genetic material generating much lower differentiation among contemporary populations compared with the Bronze Age. A cautionary tale for interpreting patterns of contemporary variation

Population Turnover: A continuing process

Several 'centers of renewed expansion' are visible across Europe in the archeological record, and several of these areas map closely to the centers of Y chromosome subclade foci

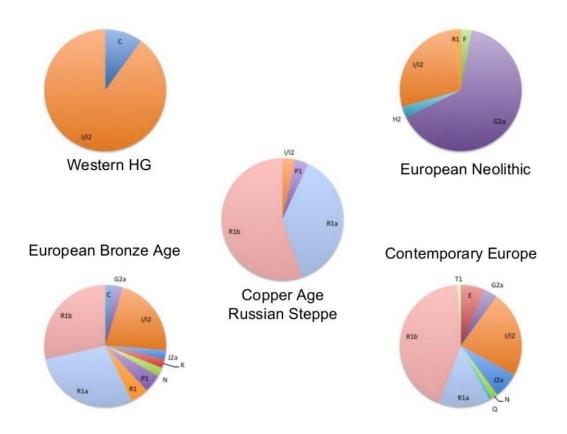


45. Several 'centers of renewed expansion' are visible across Europe in the archeological record, and several of these areas map closely to the centers of Y chromosome subclade foci Population Turnover: A continuing process L21 U152 U106



A Big Thanks to Rui Hu

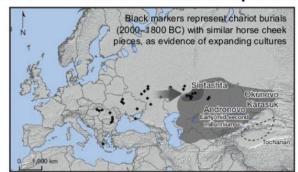
46. A Big Thanks to Rui Hu



47. Copper Age Russian Steppe Western HG European Neolithic European Bronze Age Contemporary Europe

Archeology & Genomics Converge: Post-Neolithic Cultural Expansion





- By 3000 BC, Neolithic farming cultures in Eastern Europe appear to be largely replaced by Early Bronze Age Yamnaya culture, which is associated with completely new perception of family, property and personhood, rapidly stretching from Hungary to the Urals.
- By 2800 BC Corded Ware, Single Grave or Battle Axe cultures with new social and economic formations developed in Europe, culturally replacing the remaining Neolithic farmers
- From the beginning of 2000 BC, new class of master artisans known as the Sintashta culture emerged in the Urals, building chariots, breeding and training horses, and producing sophisticated new weapons. These innovations quickly spread across Europe and into Asia

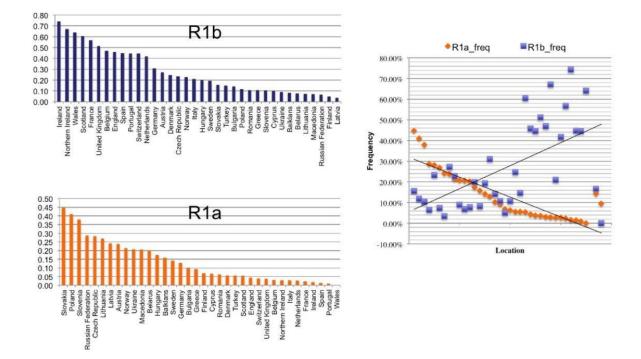
48. Distribution of Early Bronze Age cultures with arrows showing the Yamnaya expansions Black markers represent chariot burials (2000–1800 BC) with similar horse cheek pieces, as evidence of expanding cultures

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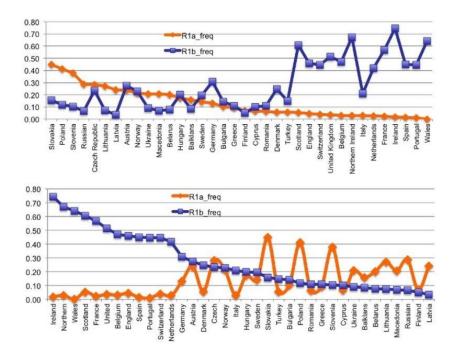
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49. (part 1) Opposite Trends: European Frequencies of R1b & R1a R1b R1a



50. (part 2)