

KUNSKAPSKRYSSNING 2019



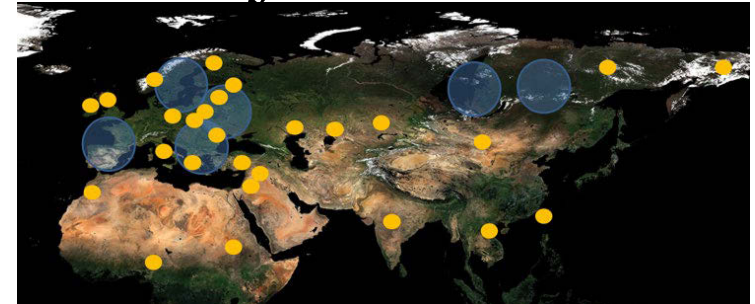
Genetik och gamla ben



Avsikten bakom projekten



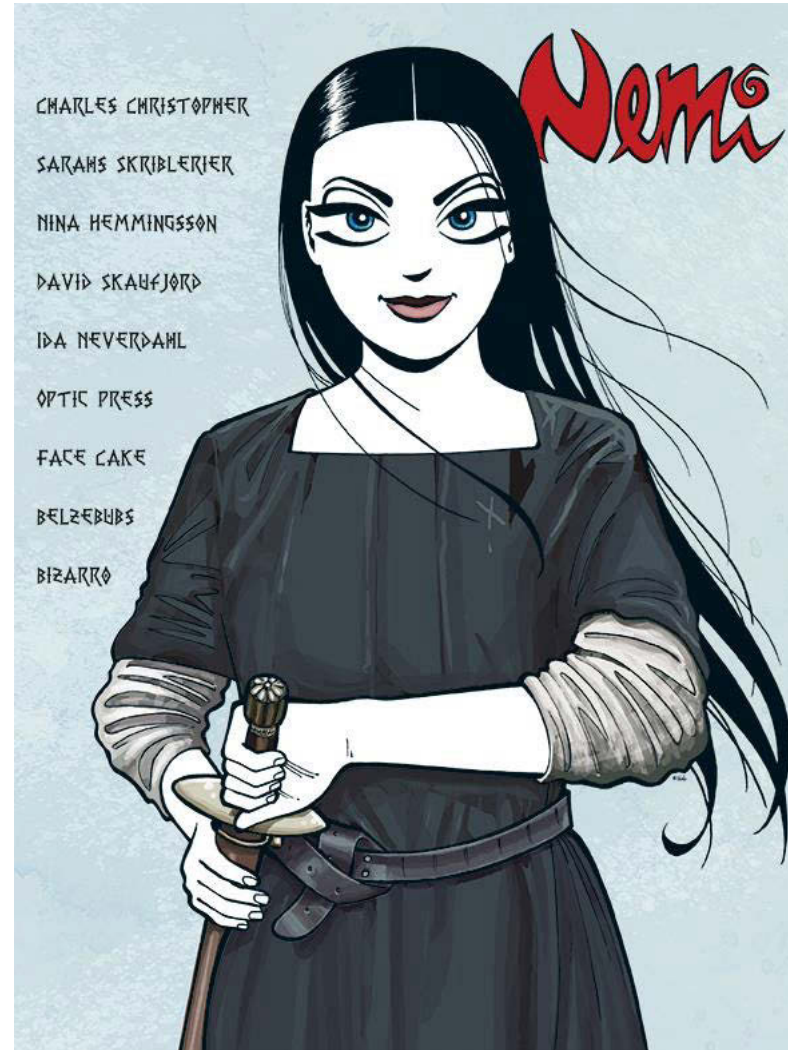
- Att göra det vi verkligen vill göra, varken mer eller mindre.
- Att söka forskningsstöd för allt vi i så fall behöver göra.
- Att genomföra projektet med de forskare vi har störst förtroende för.
- Genom tre olika forskningsprojekt undersöker vi arkeogenetiken i hela Eurasien.
- Arkeologer, genetiker, och specialiseringar mittemellan dessa jobbar i projekten.



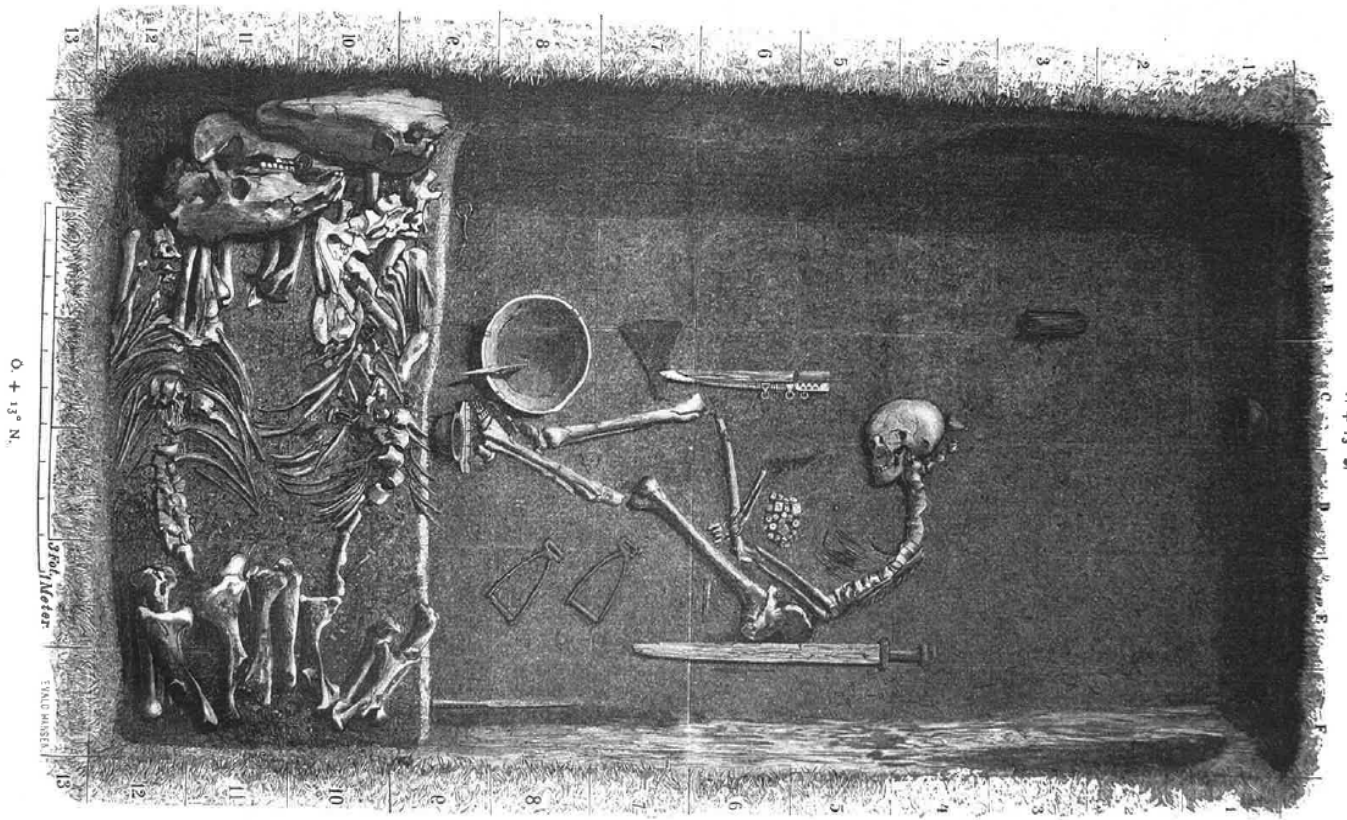
Men är det vi gör spännande?

Eller slösar vi bara bort forskningsmedel?

Låt oss titta på ett exempel (jag kommer mest tala om stenåldern, men det här är från järnåldern).



Krigarkvinnan från Birka

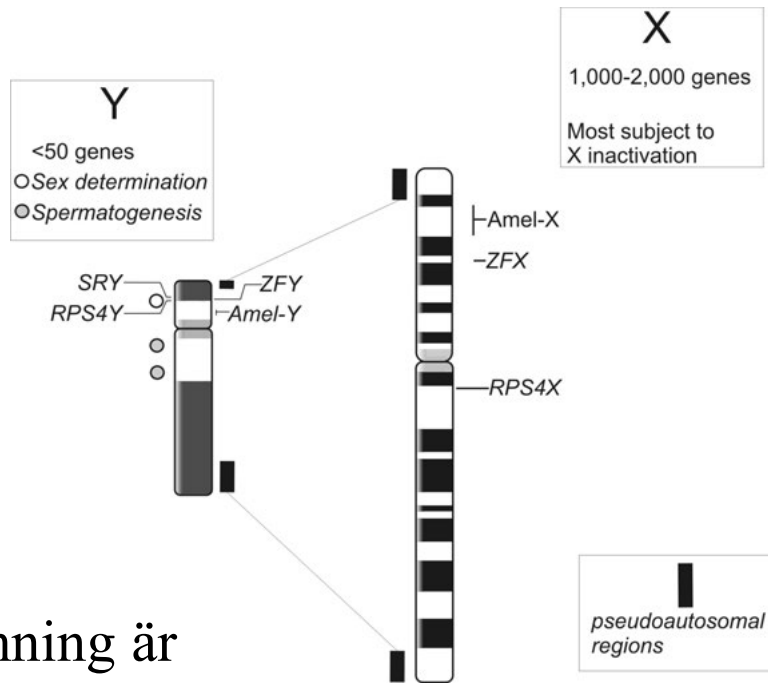


Graven (Bj581) grävdes ut 1878 och innehöll en fantastisk krigarutrustning. Sedan dess har den använts som typ-exemplet för en vikingatida krigsman.

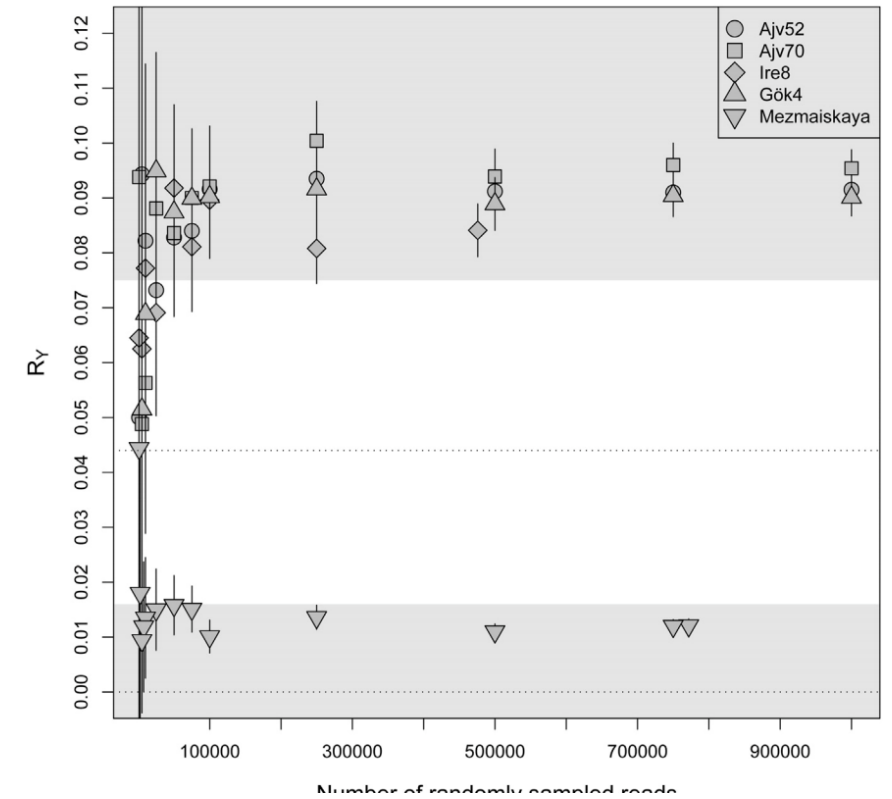
“Allt som fanns i graven var dödligt.”
– Charlotte Hedenstierna-Jonson

Hedenstierna-Jonson et al. 2017

Krigarkvinnan från Birka



En genetisk könsbestämning är en av de minst krävande analyserna. Det behövs inte mycket DNA för att genomföra en sådan.



Skoglund et al. 2013

Krigarkvinnan från Birka



Hedenstierna-jonson et al. 2017

Lavin-artad uppmärksamhet!

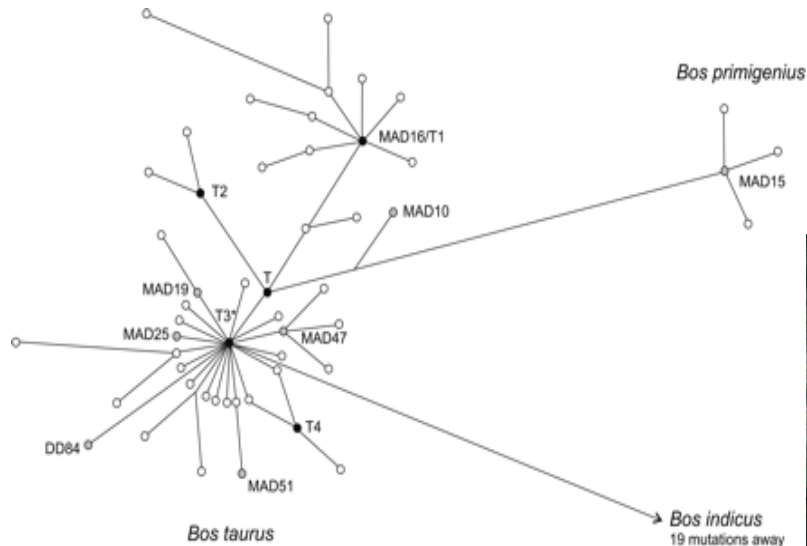
- Av 12 miljoner vetenskapliga publikationer som spåras blev vår krigarkvinna den 265 mest lästa på någon vecka.
- Mer än 130 internationella nyhetsbyråer uppmärksammade henne.
- Hon diskuterades på 2200 personliga sociala-media-sidor.

Men varför tog det oss 140 år att se henne?

Genomik-revolutionen



2005

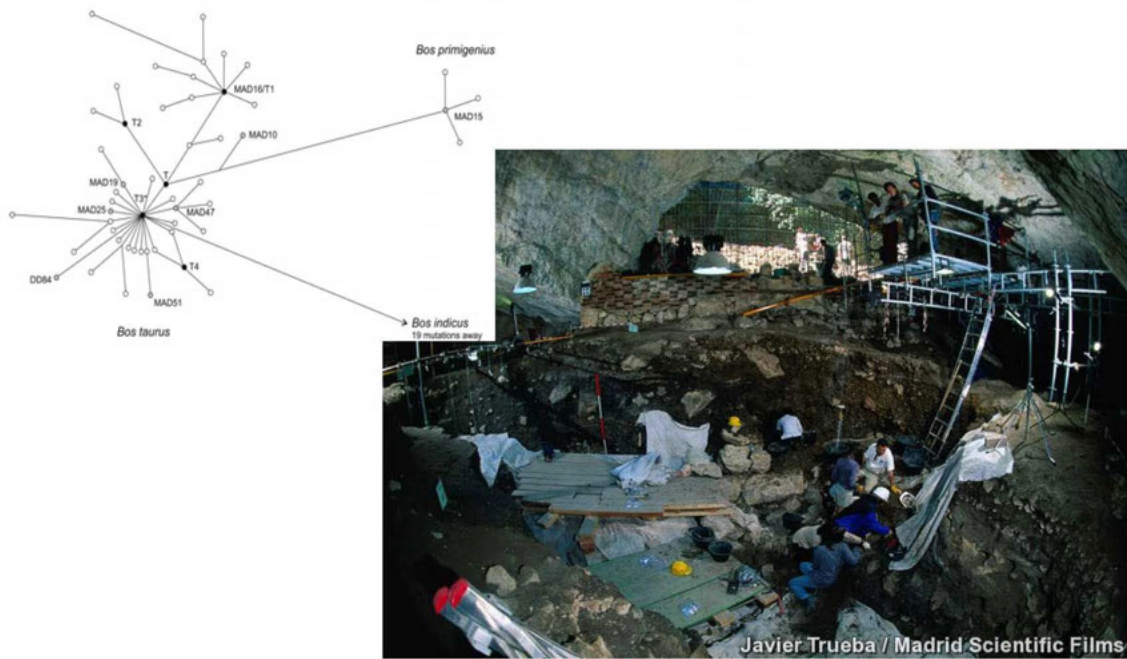


Anderung et al. 2005

Mt DNA av afrikansk typ dök upp i senneolitiska ben från en grotta i norra Spanien. Ett bevis på stenålderskontakter över Gibraltar.



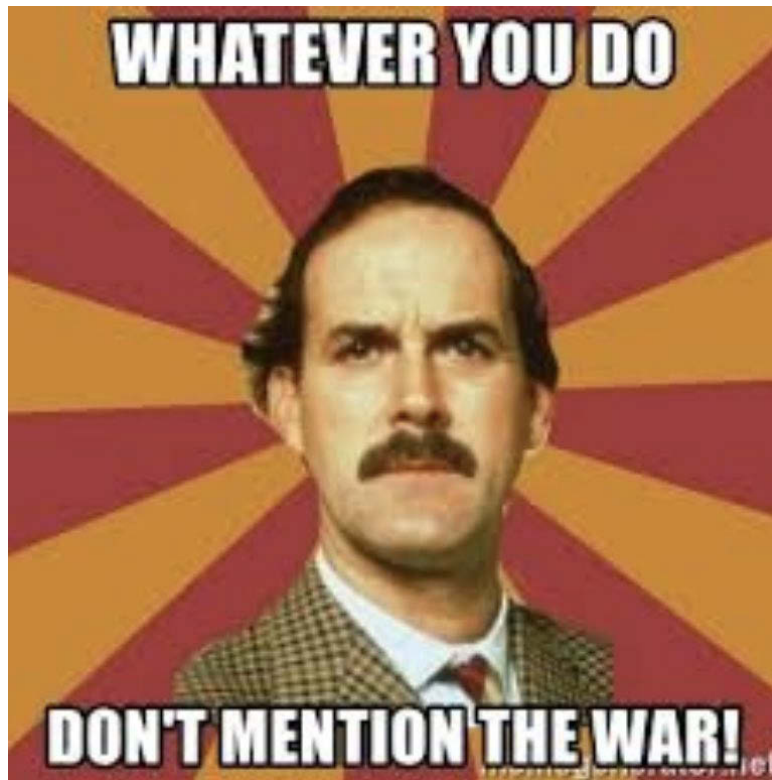
Javier Trueba / Madrid Scientific Films



Det här var bra grejer 2005,
publicerades i PNAS

- 24 individer
- Inte människor (boskap)
- Mindre än 300bp/individa (0.00001% av ett genome, 0.000001X)

De två sakerna som var tabu i aDNA (på den tiden)



- Bärnstens DNA



- Förhistoriskt humant DNA



Nu för tiden publicerar vi sådana mängder DNA som skulle varit science fiction för 10 år sedan

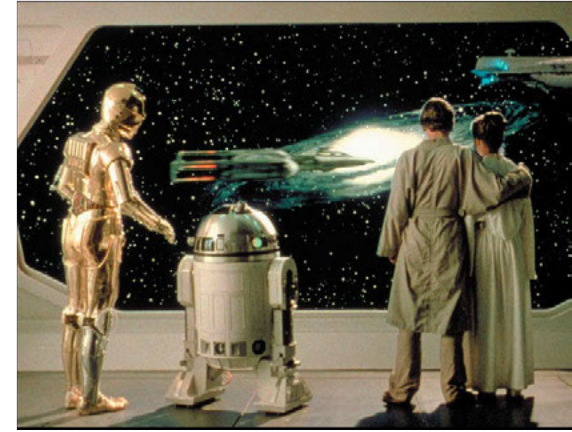
Individual	Calibrated date (cal BP, 2 sigma)	Genome coverage	mt coverage	Sex	mt haplo-group	Y haplo-group	Contamination estimate		
							based on mt	based on X	based on autosomes
Hum1	9452-9275 ^{\$}	0.71	597	XX	U5a1	-	0.29%	-	0.00%
Hum2	9452-9275 ^{\$}	4.05	432	XY	U5a1d	I2-L68	0.15%	0.63%	0.73%
Steigen	5950-5764	1.24	277	XY	U5a1d	I2a1b-M423	0.00%	0.4%	0.00%
SF9	9300-8988	1.15	93	XX	U4a2	-	5.36%	-	0.00%
SF11	9023-8760	0.10	45	XY	U5a1	*	3.42%	*	10.16%
SF12	9033-8757	57.79	9774	XX	U4a1	-	0.34%	-	0.932%
SBj	8963-8579	0.43	102	XY	U4a1	I2-L68	3.72%	1.4%	0.06%

^{\$} combined probability for the Hummervikholmen samples

* not enough genome coverage

Günther et al. 2018

“A new hope”



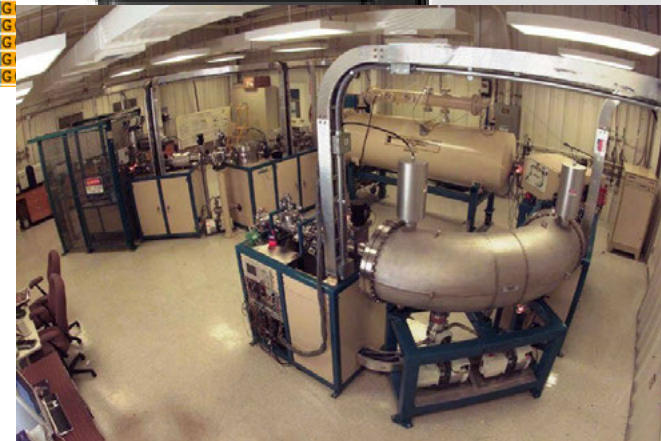
- . Storskalig parallell sekvensering
- . >300.000 fragment på 100bp (tidig teknik)
- . Tekniken publicerades **2005**, de första dataseten **2006**.

Vattnet i ett glas jämfört med vattnet i Östersjön



Våra data

Gallirallus australis	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus australis australis	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus australis greyi	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus calayanensis	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus insignis 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus insignis 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus lafresnayanus	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus modestus 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus modestus 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus owstoni 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus owstoni 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis assimilis	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis mellori 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis mellori 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis philippensis 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis philippensis 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis sethsmithi 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis sethsmithi 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus philippensis yorki	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus roivanae 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus roivanae 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus striatus 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus striatus 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus striatus 3	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus sylvestris 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus sylvestris 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus torquatus celebensis	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus torquatus sulcirostris	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus torquatus torquatus 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus torquatus torquatus 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus wakensis 1	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG
Gallirallus wakensis 2	AACTCCAGCCAAAGGAGCCATCTCTCATCGATCTACCTACACATG

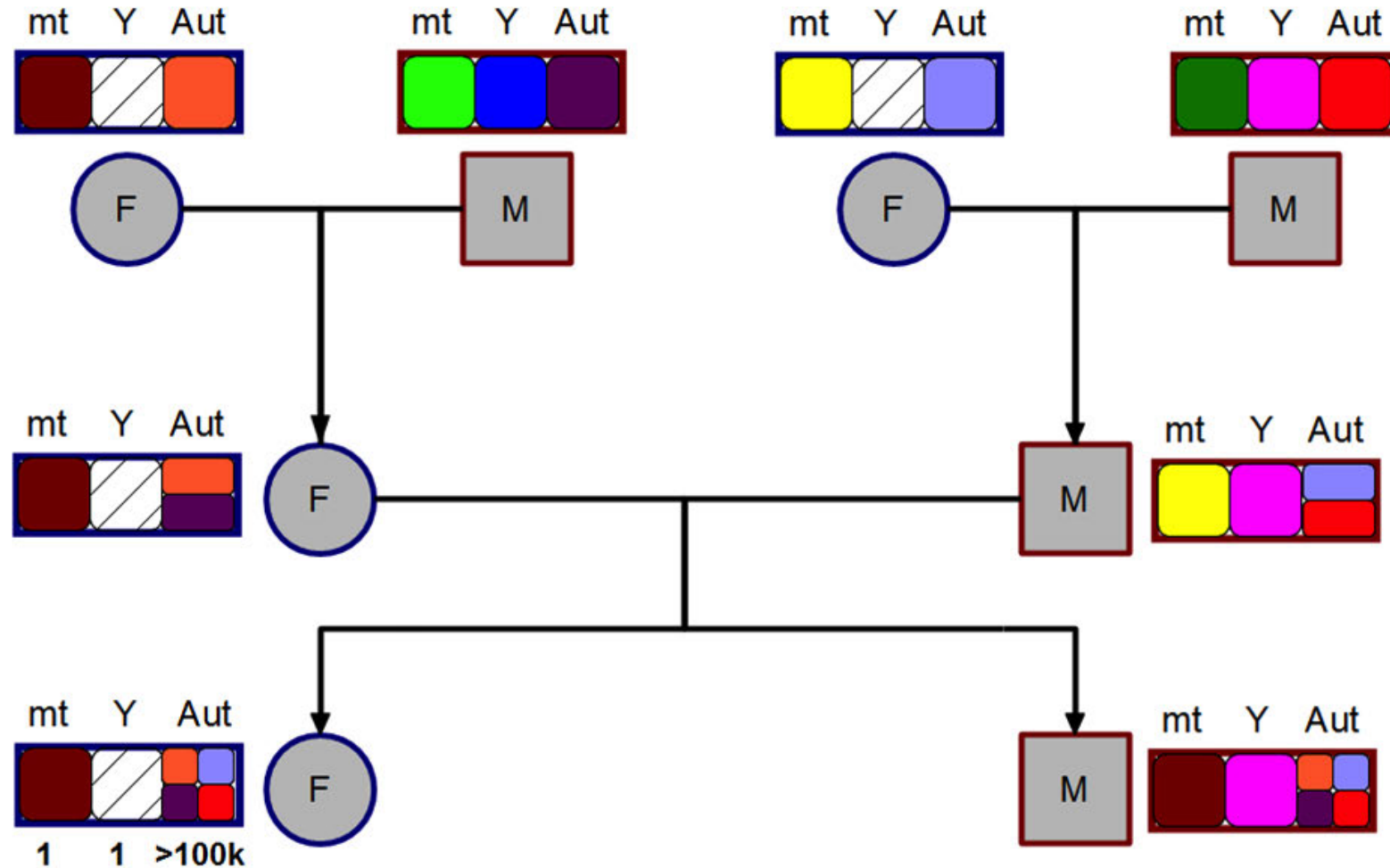


Sr

Arvsgångarna

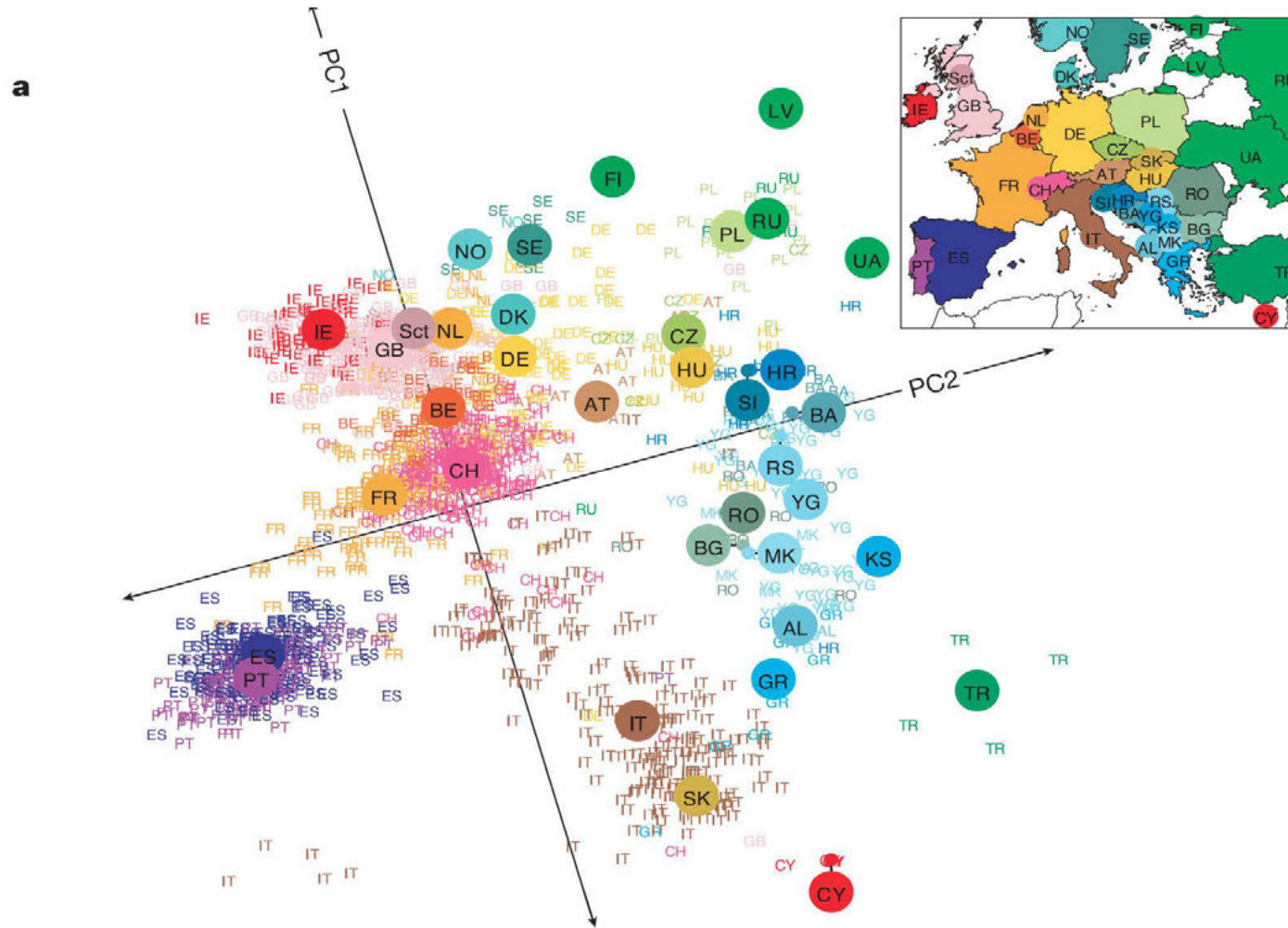
Generation

1
↓
2
↓
3



Number of locus

Substruktur – “isolation by distance”

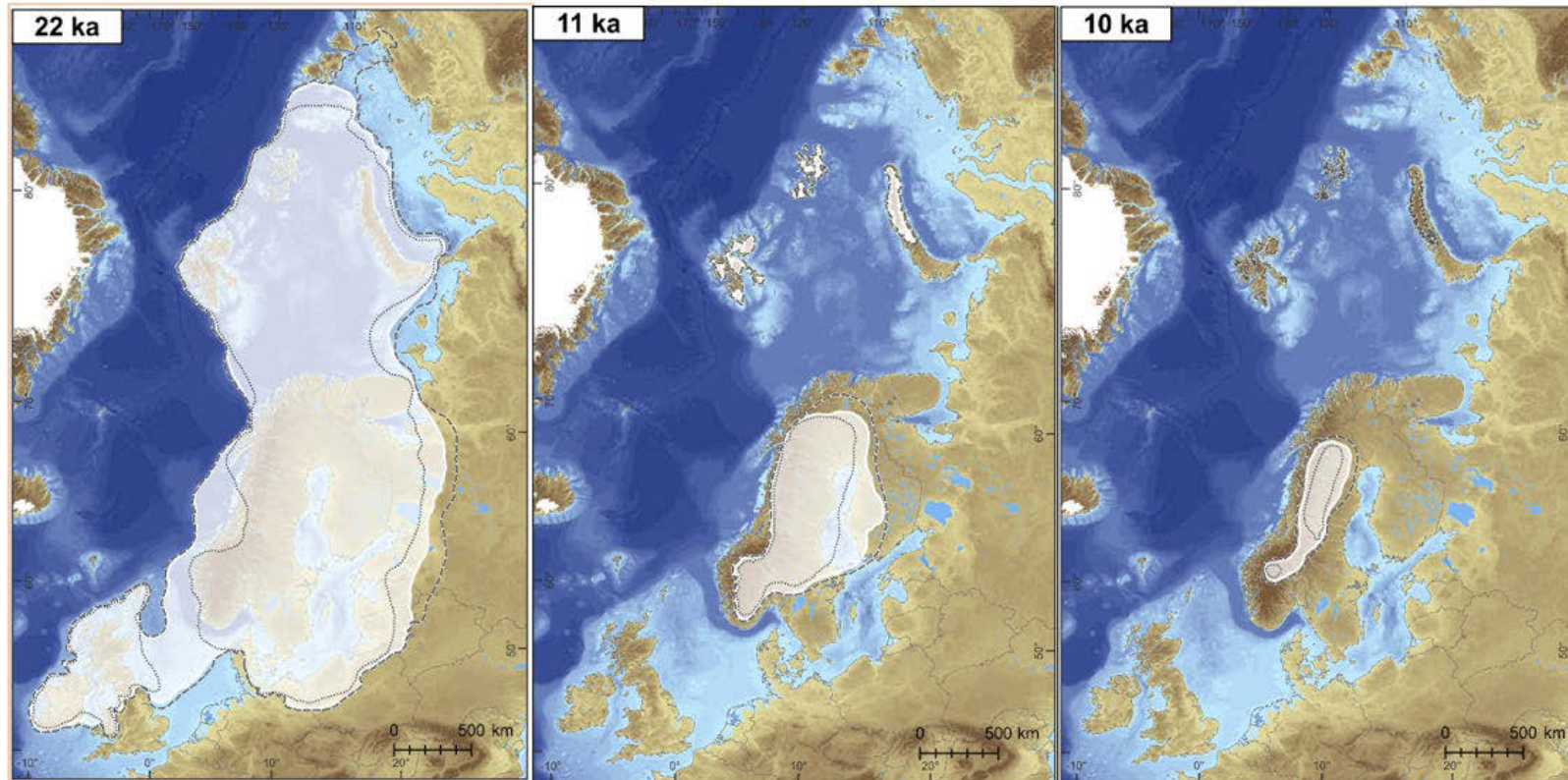


Arrhenius ekvationens konsekvenser, DNA är som glass



- Så länge den står i frysen är allt bra och alla glada.
- Tar man ut den ur frysen blir det kladdigt och rörigt rätt fort.

Vilka var de första skandinaverna?



Mesolitiskt material



Från Norge och Gotland

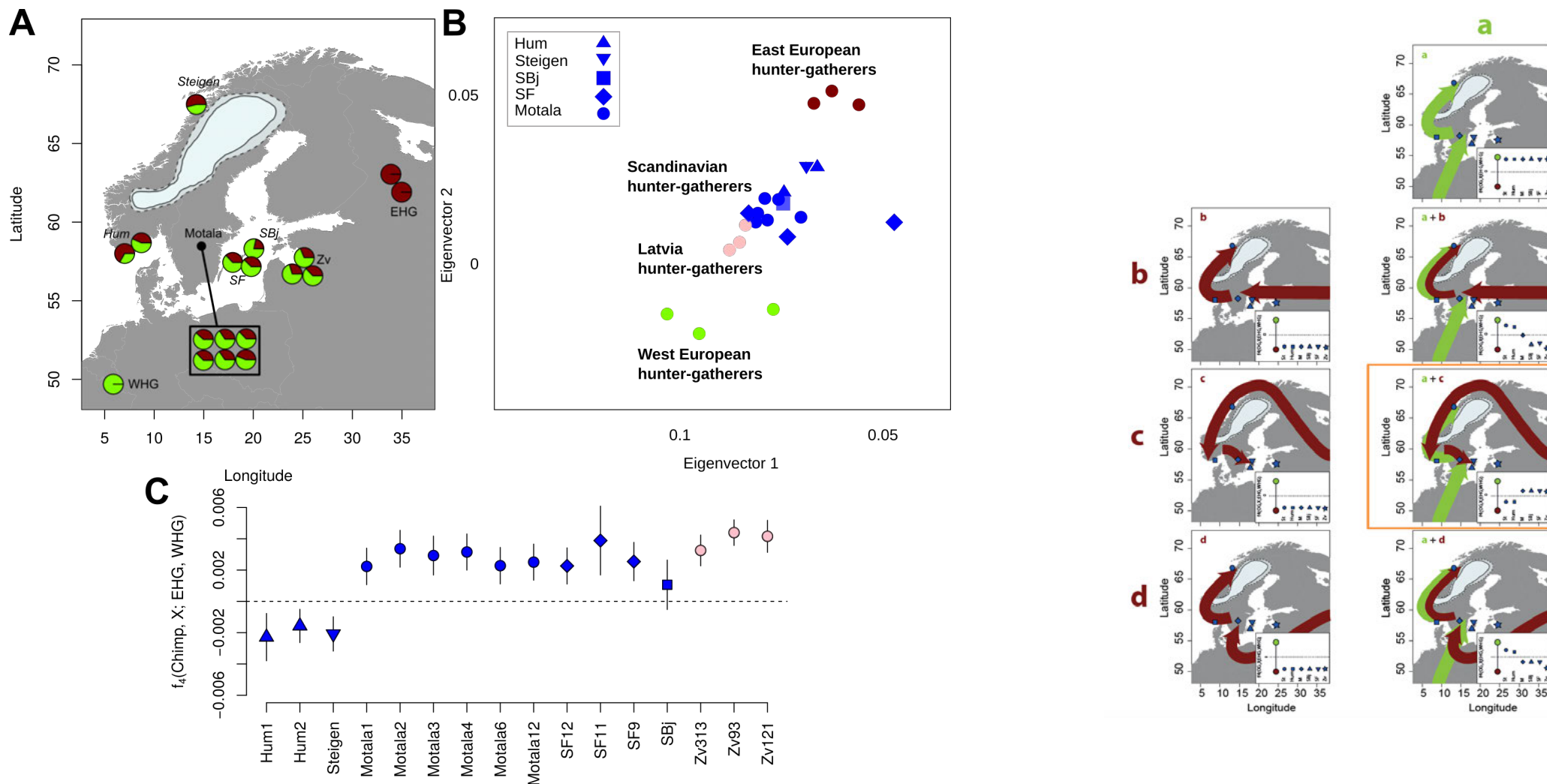
Mesolithic materials, some statistics

Individual	Calibrated date (cal BP, 2 sigma)	Genome coverage	mt coverage	Sex	mt haplo-group	Y haplo-group	Contamination estimate		
							based on mt	based on X	based on autosomes
Hum1	9452-9275 ^{\$}	0.71	597	XX	U5a1	-	0.29%	-	0.00%
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SF9	9300-8988	1.15	93	XX	U4a2	-	5.36%	-	0.00%
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^{\$} combined probability for the Hummervikholmen samples

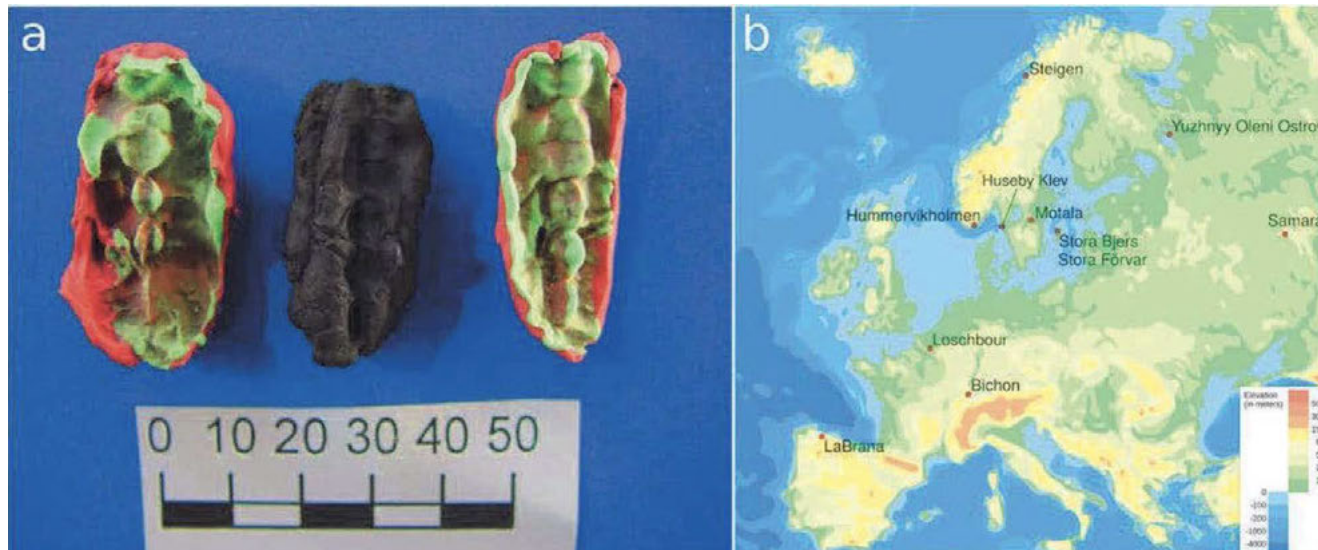
* not enough genome coverage

East and west, a paradox



Günther et al. 2018

Mesolithic chewing gums



Metagenomics, the boy from Huseby-Klev was not feeling too well.

Material	Age	Strategy	Species	Reads
Resins, Huseby-Klev	9880-9540	Alignment	<i>Rothia mucilaginosa</i>	737 039
			<i>Gemella sanguinis</i>	348 738
			<i>Rothia dentacariosa</i>	345 172
			<i>Treponema denticola</i>	10 055
			<i>Tannerella forsythia</i>	6 550

The Neolithisation



Passage tomb in Haväng

The Neolithisation – the transition from a hunter-gathering lifestyle to a farming lifestyle

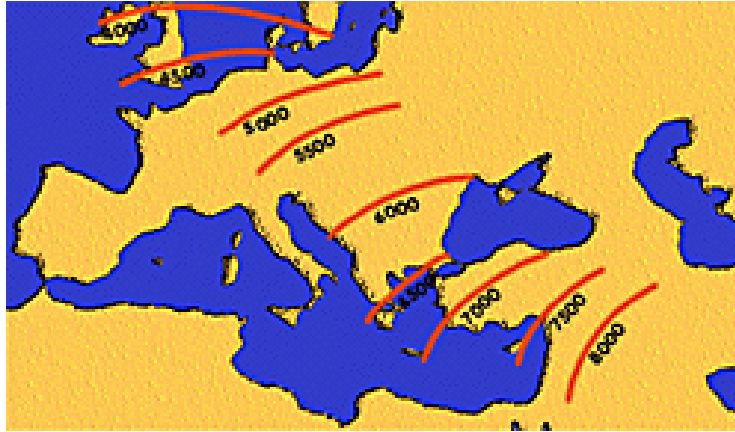
Consequences



Reconstruction of a swiss pile dwelling

- Villages and population clusters
- Social structures
- Innovations and technological advancements
- Organised warfare
- Diseases

When?



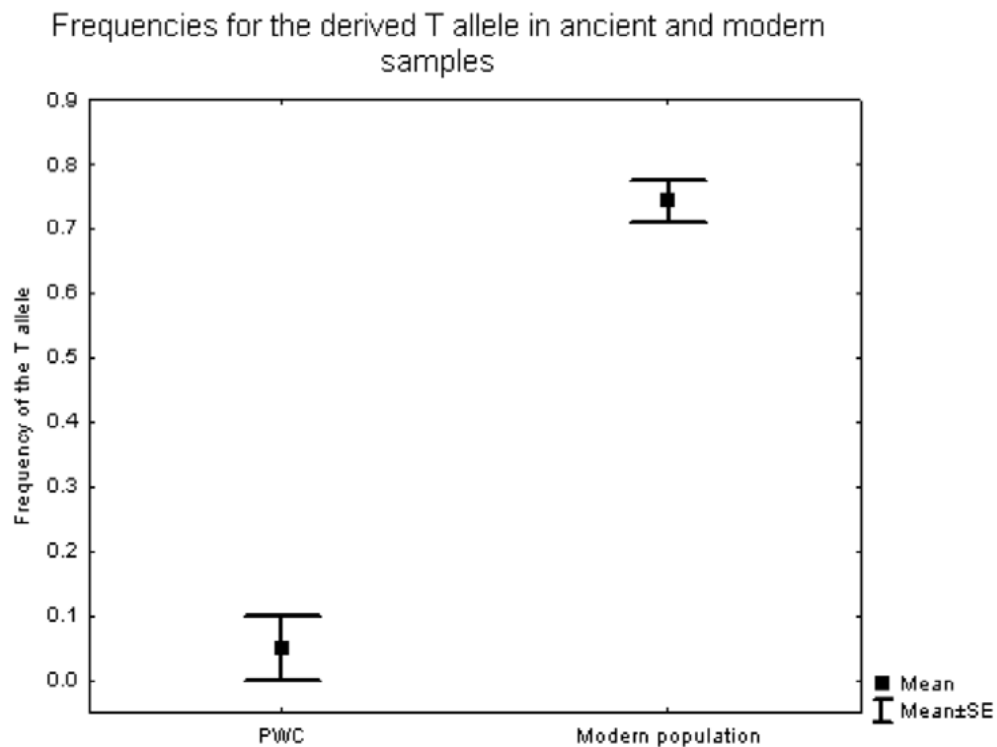
- >8000 BCE in Anatolia / the Levant
- >6000 BCE in southeastern Europe
- ~5000 BCE in northern Europe
- ~4000 BCE in Scandinavia

Pre-2012 Neolithisation genetics

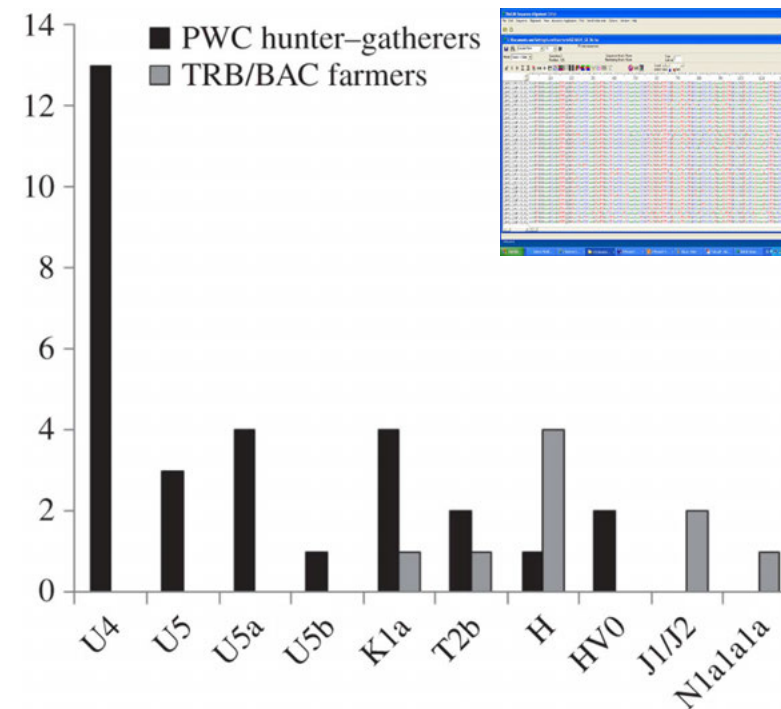


Lactase intolerance
(-13910)

Different mt haplogroups

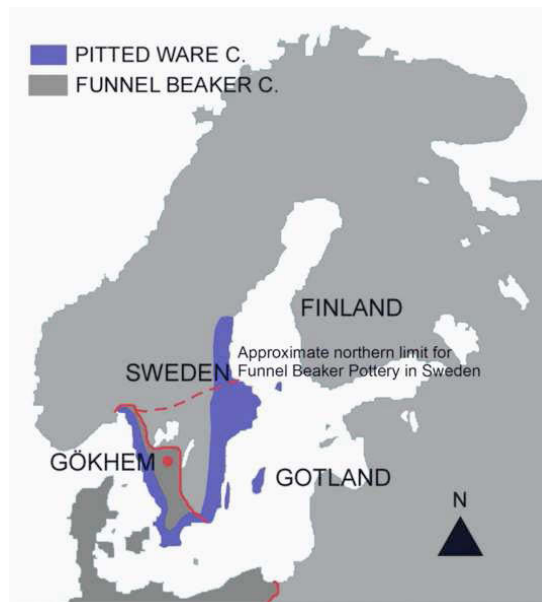


Malmström et al. 2010



Malmström et al. 2009

Sampling parallel systems in Sweden



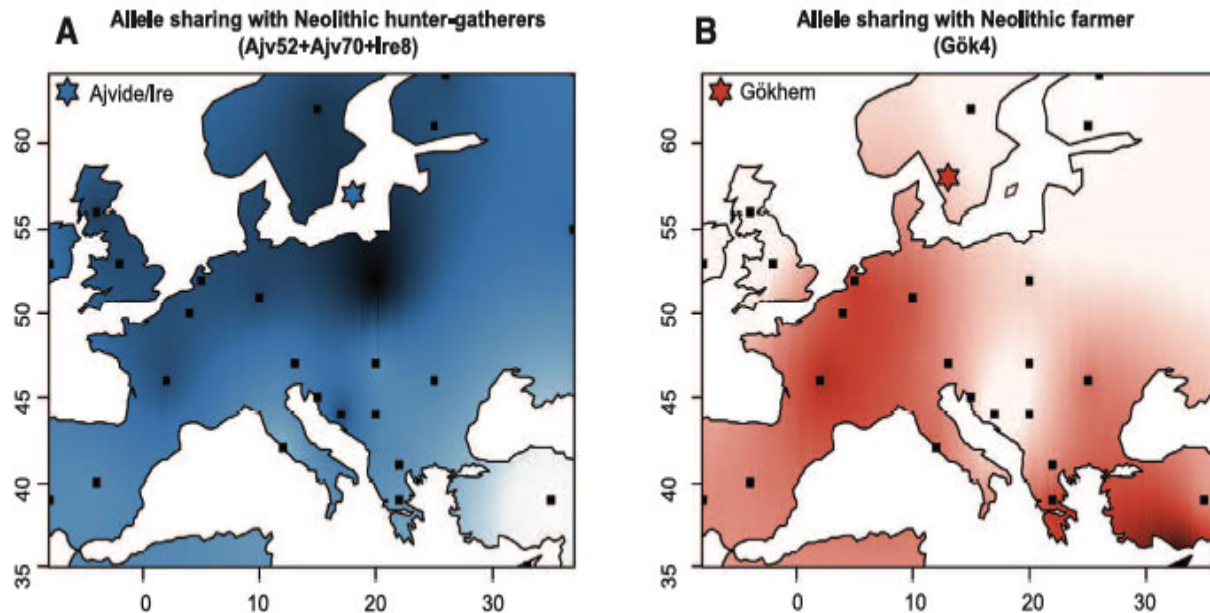
Three late hunter-gatherers from the Baltic island Gotland, and one early farmer (early in a Scandinavian context...) from central Sweden.

					Genotyped SNPs			mtDNA genome assembly	
Sample	Archaeological context	Fraction of human sequence reads*	Human autosomal sequence reads†	Human autosomal sequence data (bp)‡	HM3+ FINHM+ HGDP§	FINHM+ POPRES§	1KGPomni§	Mean depth	mtDNA haplogroup
Neolithic hunter-									
Ajv52	gatherer	2.38%	1,029,854	59,563,626	7,531	4,189	23,123	14.0X	V
Ajv70	"	4.85%	1,659,553	97,210,801	12,193	6,824	39,014	13.8X	U4d/U4a2
Ire8	"	2.71%	601,416	26,843,368	3,279	1,905	10,273	9.8X	U4d
Gök4	Neolithic farmer	6.31%	1,208,835	65,535,732	7,712	4,413	24,311	4.2X	H

*Nonredundant reads mapping to the human genome in libraries amplified by Phusion polymerase. †Mapping quality ≥ 30 , nonredundant autosomal data only. ‡Mapping quality ≥ 30 , base quality ≥ 15 , nonredundant autosomal data only. §See Fig. 1 legend and (16) for an explanation of abbreviations.

The genetic distance was massively larger than the geographic!

1658 SNPs



But those were not really Mesolithic dudes, and just one farmer, Anders is just doing story-telling...

Skoglund et al. 2012

And there was also another problem...

The farmers were supposed to be from the Levant or Anatolia



But it looked as if they originated from Sardinia



More individuals, higher coverage

Sample	Context	Genome coverage	mtDNA coverage	mtDNA hg	Contam. (95% CI)	Source	Age CalBP*	Genetic sex
StoraFörvar11	Mesolithic	0.09	25.6	U5a1	0-22.2%	This study	7,500-7,250	Male
Ajvide52	PWC	0.09	49.4	V	0-3.7%	This study and (8)	4,900-4,600	Male
Ajvide53	PWC	0.03	2.5	U4d	-	This study	4,900-4,600	Female
Ajvide58	PWC	2.22	161.7	U4d	0-0.6%	This study	4,900-4,600	Male
Ajvide59	PWC	0.01	1.3	U	-	This study	4,900-4,600	Male
Ajvide70	PWC	0.16	52.5	U4d	1.5-7.7%	This study and (8)	4,900-4,600	Male
Ire8	PWC	0.04	43.2	U4d	1.6-9.6%	This study and (8)	5,100-4,150	Male
Gökhem2	TRB	1.33	91.9	H1c	0-2.7%	This study	5,050-4,750	Female
Gökhem4	TRB	0.04	6.5	H	0-25.9%	(8)	5,280-4,890	Male
Gökhem5	TRB	0.02	26.2	K1e	0-4%	This study	5,050-4,750	Female
Gökhem7	TRB	0.01	32.8	H24	0-7.6%	This study	5,050-4,750	Female

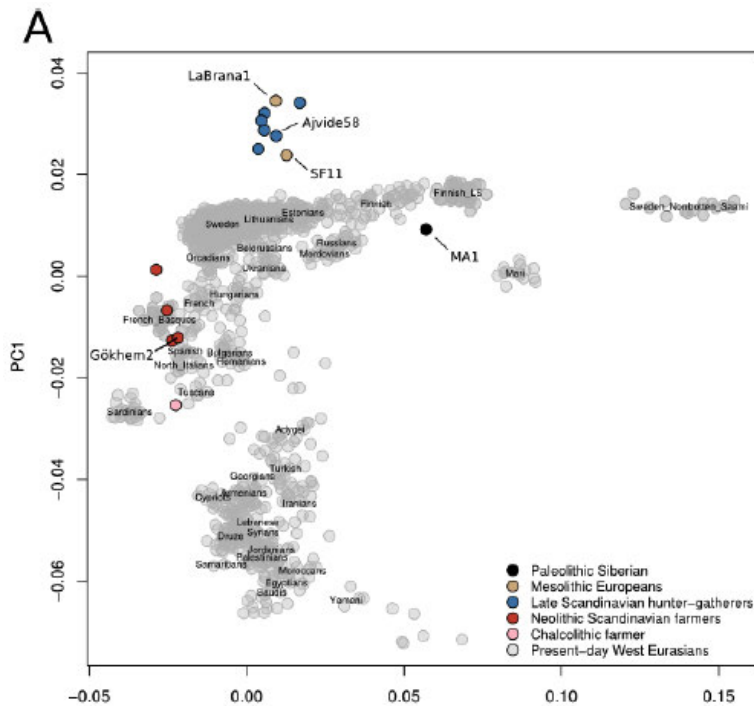
Skoglund et al. 2014

“But the story remains the same, if you take a look...”

-Yazoo

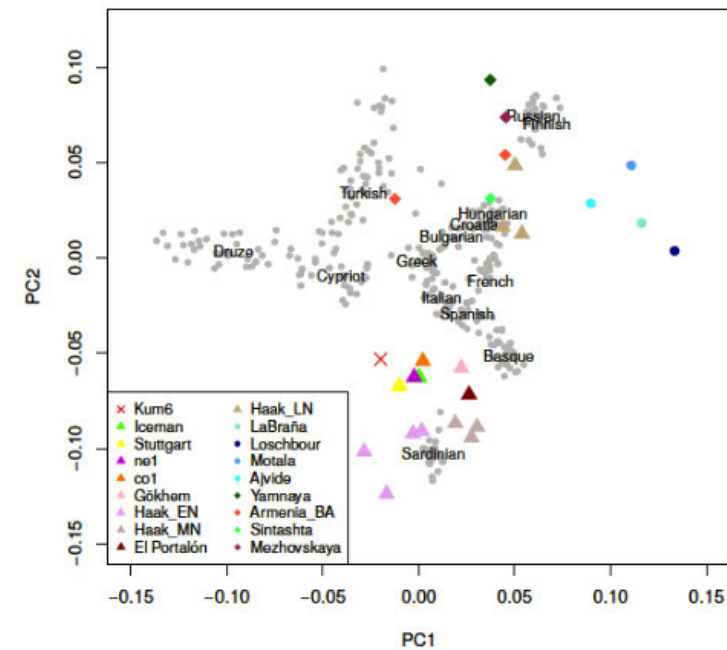


Two distinct groups



Skoglund et al. 2014

And with an Anatolian sample



Omtrak et al. 2016

Even more Anatolian samples are just telling the same story.

Coverage

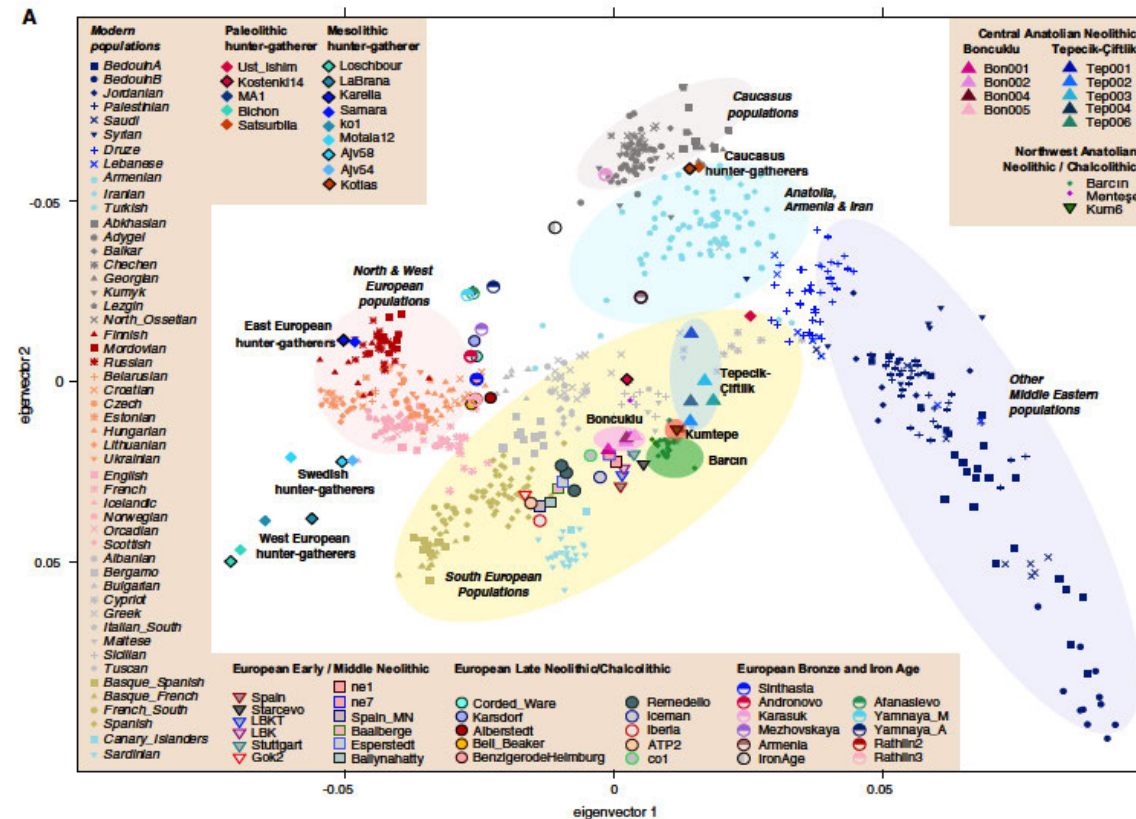
Table 1. Summary Statistics of the Sequencing Data for Nine Ancient Individuals

Sample	Genome Coverage	mtDNA Coverage	Read Length (Mean)	mtDNA Haplogroup	Genetic Sex
Bon001	0.166	654.604	63.208	U3	XY
Bon002	6.688	2,379.090	69.841	K1a	XX
Bon004	0.243	351.234	70.703	N1a1a1	XY
Bon005	0.039	68.615	71.021	N1a1a1	XX
Tep001	0.023	66.812	80.863	K1a	XY
Tep002	0.721	730.833	60.814	K1a12a	XX
Tep003	0.694	281.963	60.849	N1b1a	XY
Tep004	0.473	391.608	61.473	N1a1a1	XX
Tep006	0.267	259.879	83.585	N1a1a1	XY

See [Data S2](#) for summary statistics for each library and for SNPs used for haplogroup classification.

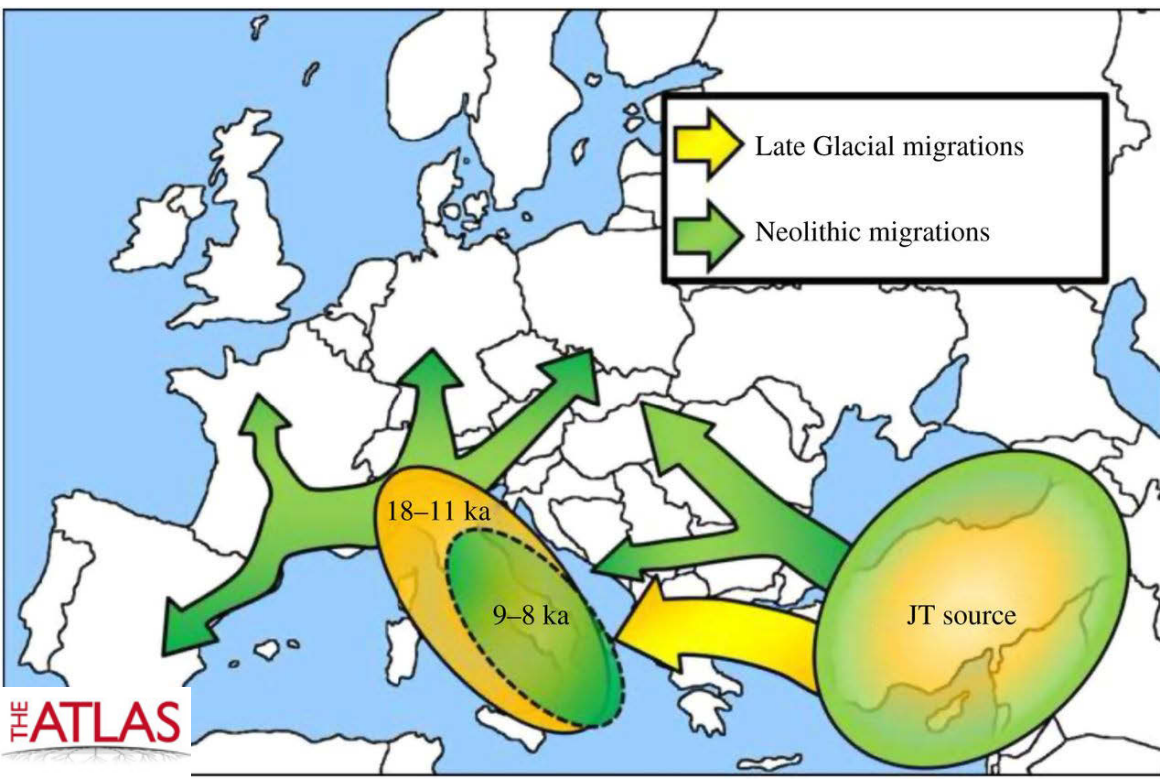
Kılınç et al. 2016

Clustering



The Neolithisation

Malmström et al. 2009, Skoglund et al. 2012, Skoglund et al. 2014, Omrak et al. 2016

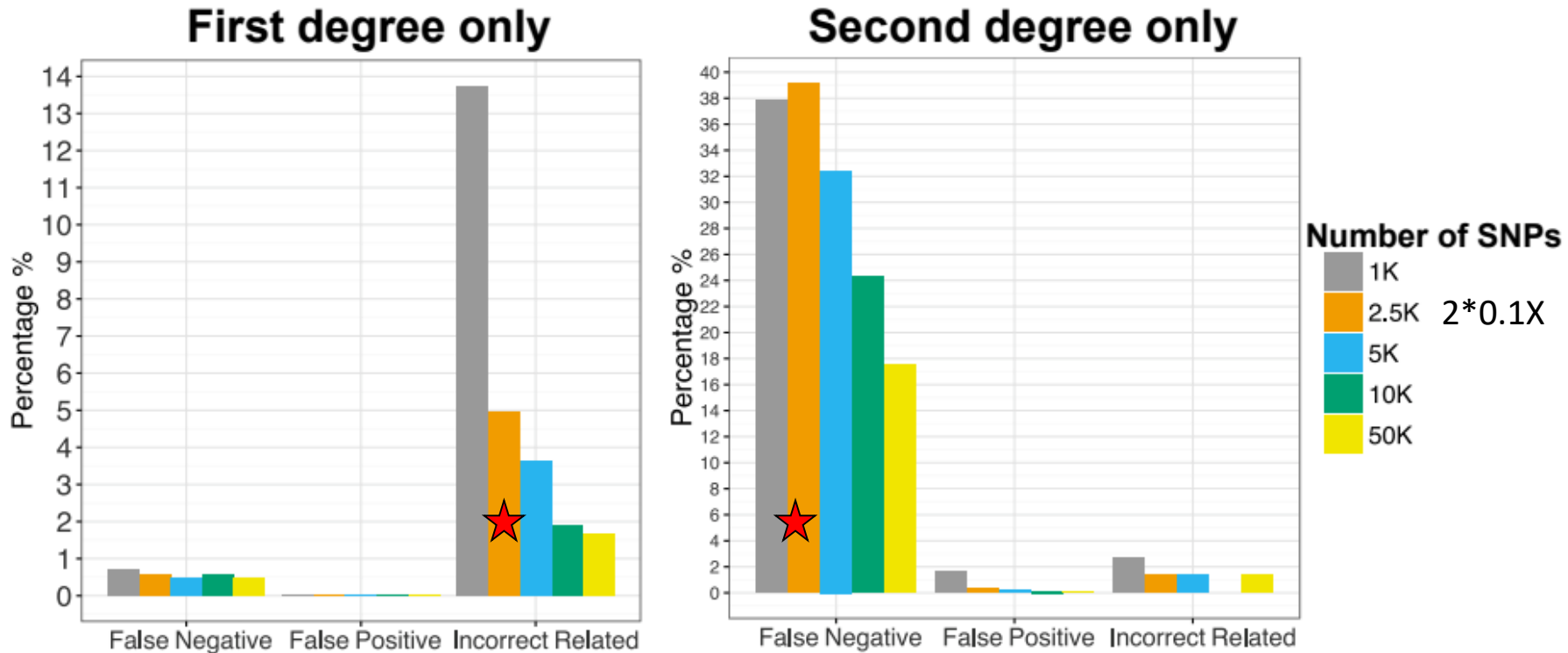


The Neolithisation of Europe, it started from the Near East and had a significant impact on all of Europe.

In Scandinavia the new genetics is tightly connected to the Funnel Beaker Complex (TRB).

Kinship

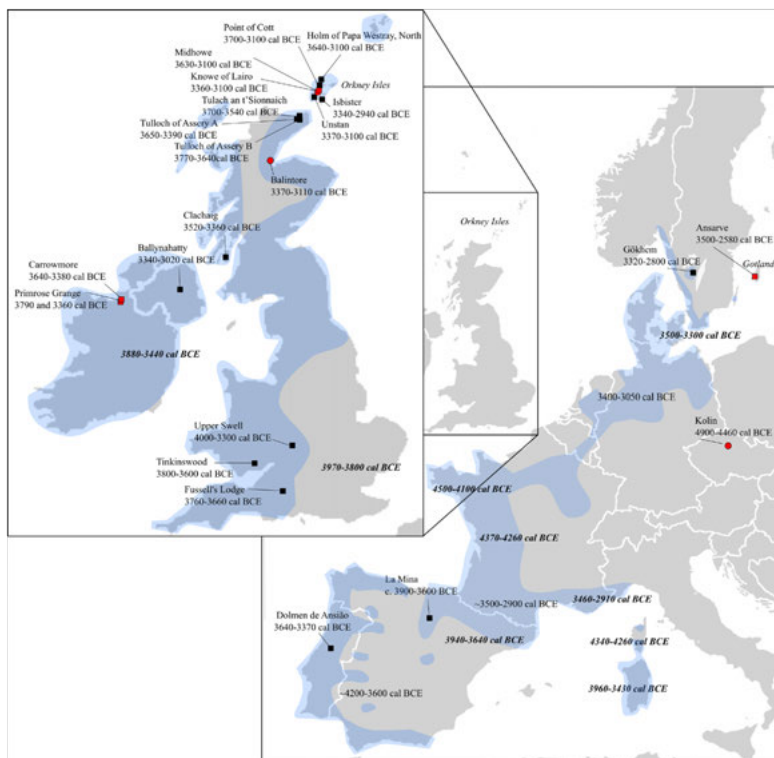
READ (Relationship Estimation from Ancient DNA)



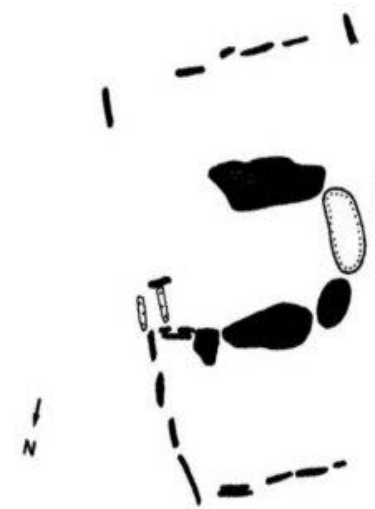
★ 2*0.1X will reveal siblings, but perhaps miss cousins

Kinship in the megaliths

On Ireland and on Gotland



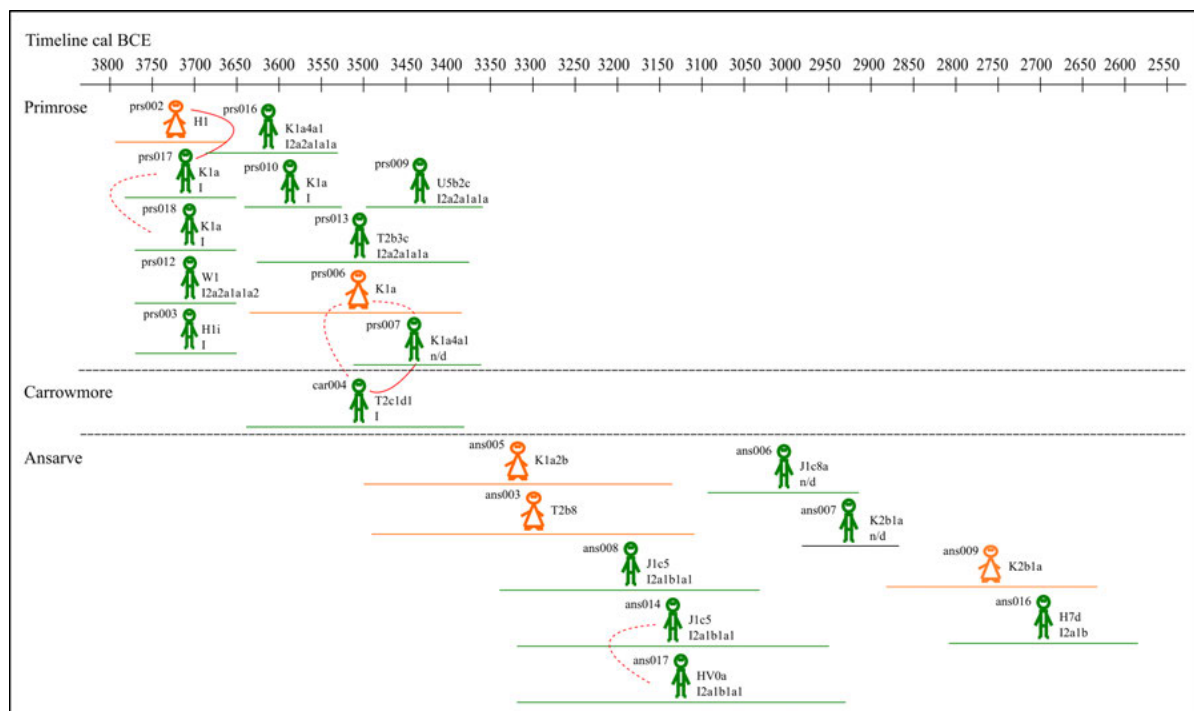
On Gotland



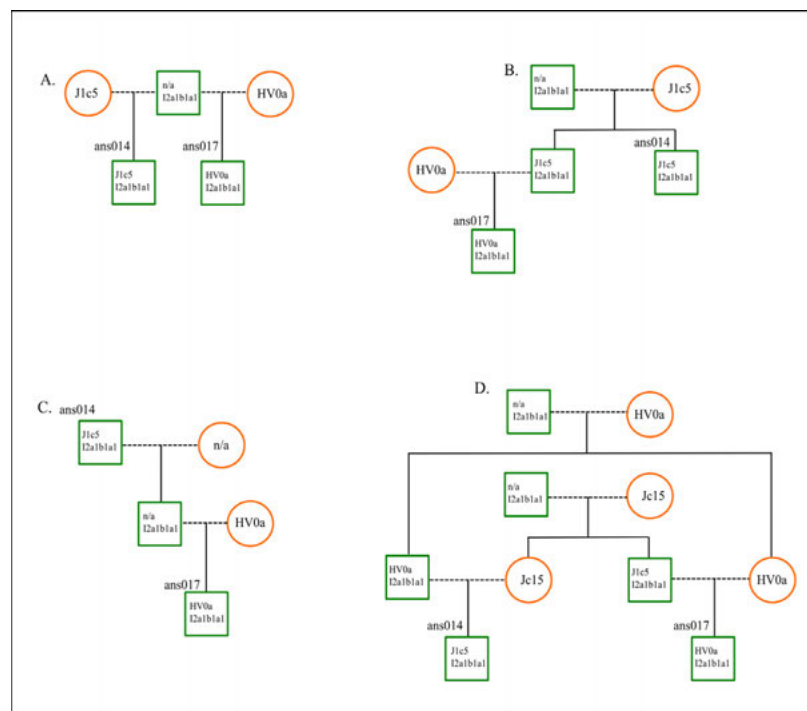
Sanchez-Quinto et al. 2019

Kinship in the megaliths

On Ireland



And on Gotland



Sanchez-Quinto et al. 2019

The Research group

half public (RJ, VR), half
private (KAW)



Maja



Torun



Anna



Jan



Vendela



Yours truly

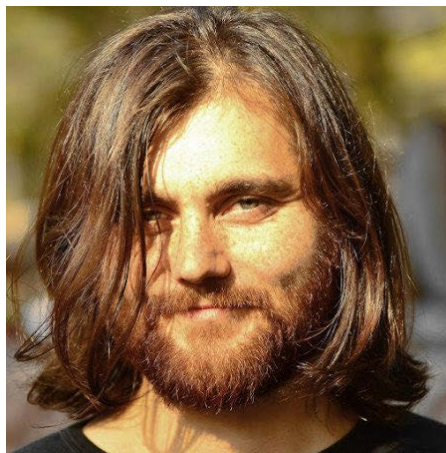
Emrah

David

Gulsah

Dalia

Ricardo



“I don’t know where I’m going from here, but I promise it won’t be boring”

-David Bowie

