

:: Marker Testing ::

To determine which haplogroup you are in, your DNA was first extracted from the sample you provided. It then underwent a primary screen which looks at several SNP markers at the very top of the Y-chromosome tree. This primary panel, called Multiplex A-R, is listed below along with the secondary panels. Based upon the results of this primary screen, the secondary panel was chosen. The panels that you were tested upon are marked light blue and the markers that you were positive on shown light green.

Multiplex	A-R	AB	CD	E	FGHI	J
Region covered	All	African (for 168C samples)	Asian (for M168T/M89C/M96G samples)	African, Middle Eastern (for M96C samples)	Eurasian (for M89T/M9G/M304A samples)	Middle Eastern (for M304C samples)
Markers Tested	M9	M31	M15	DYS391	M26	M47
	M45	M32	M38	M2	M52	M67
	M89	M42	M48	M33	M170	M92
	M96	M150	M55	M35	M201	M172
	M122	M146	M125	M58	M253	M241
	M168	M182	M130	M75	P15	M267
	M175	P4	M131	M78	P16	
	M207		M145	M81	P37	
	M304		M151	M123		
	M343		M210			
	AmelXY		M217			

Multiplex	KLMN	O1	O2	PQ	R1	R2
Region covered	Eurasian (for M9C/M45G/M175+ samples)	SE-Asian (for M175-/M122T samples)	SE-Asian (for M175-/M122C samples)	Asian, Native American (for M45A/M207A samples)	Indo-European (for M207G/M343C samples)	Indo-European (for M343A samples)
Markers Tested	M5	M88	M7	M3	M17	M18
	M11	M95	M113	M19	M56	M37
	M70	M101	M117	M120	M87	M65
	M178	M103	M121	M143	M124	M126
	M214	M119	M134	M194	M157	M153
	M231	P31	M159	M199	M173	M269
	SRY9138	SRY465	M164	M242	SRY10831	P25
	Tat			M323		SRY-2627

:: Haplogroup Result ::

The testing of your sample shows that you were positive on the above highlighted markers. Additionally, you were negative on the other markers within the panels tested. Knowing this we can determine your haplogroup.

We determine you to be in Y-chromosome haplogroup **I***

Y-chromosomal haplogroup I is defined by markers M170 and P19 according to nomenclature of Y Chromosome Consortium (YCC) (2002; 2003). In earlier literature this haplogroup was referred as Eu 7 plus 8 (Semino et al. 2000) or haplogroup 2 (according to nomenclature of Jobling et al. 1997; Rosser et al. 2000; Helgason et al. 2000). Although the latter 'superhaplogroup' overlaps only partly with haplogroup I, in European populations the coverage is more relevant, as majority of European haplogroup 2 individuals belong to haplogroup I according to more recent studies. Phylogeny of defining markers for haplogroup I in wider context of haplogroup F (lineages defined by M89) according to nomenclature of YCC (2002) was presented in study of Rootsi et al. (2004).

The polymorphism M170 represents a putative Palaeolithic mutation which age has been estimated to be about 22 000 years (Semino et al. 2000), similar value of about $23,000 \pm 7,700$ years was given by Rootsi et al. (2004). It has been proposed by Semino et al. (2000) that M170 originated in Europe in descendants of men who arrived from the Near East about 25 000 years ago. The initial spread of the haplogroup I carriers in Europe is usually linked to the diffusion of the largely pan-European Gravettian technology.

Gravettian is the second subdivision of the Upper Paleolithic technological phase in Western Europe (from 27,000 to 21,000 years ago). Gravettian culture earlier phase (c.28,000-23,000 ya) of the European Upper Paleolithic is characterized by a stone-tool industry with small pointed blades used for big-game hunting (bison, horse, reindeer and mammoth). It is divided into two regional groups: the western Gravettian, mostly known from cave sites in France, and the eastern Gravettian, with open sites of specialized mammoth hunters on the plains of central Europe and Russia. The most characteristic artworks made by Gravettian artists were the famous Venus figurines.

Haplogroup I-M170 is a component of the present European Y-chromosome gene pool accounting on average for 18% of the total paternal lineages and is the only major clade of the Y phylogeny, autochthonically arisen, widespread over Europe but virtually absent elsewhere, including Near East (Semino et al. 2000; Barac et al. 2003; Rootsi et al. 2004).

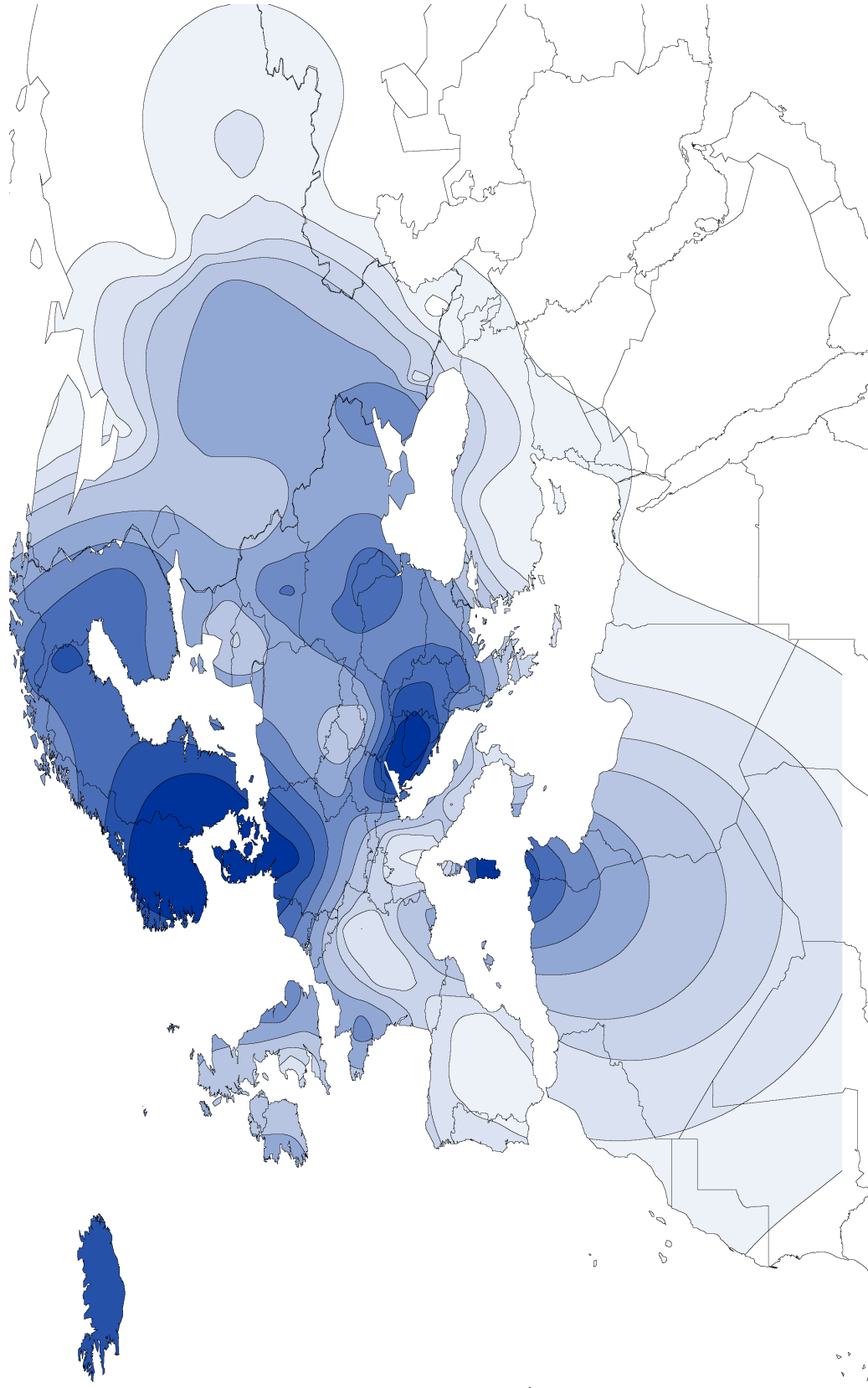
In earlier studies it has been shown that high frequency of hg I (about 40-50%) is characteristic for two distant and distinct regions of Europe - Southern Europe, around the Dinaric Alps (Barac et al. 2003; Semino et al. 2000) and in Nordic populations of Scandinavia (Tambets et al. 2004; Semino et al. 2000; Passarino et al. 2002). In other regions of Europe intermediate or low frequency is characteristic. Relatively high frequencies are characteristic also to some French regions like Low Normandy (24%) and Southern France (16%). Mostly the frequency cline is fluent, but interestingly, a lower frequency of haplogroup I distinguished the Baltic speaking Latvians from their northern neighbors, the Finnic-speaking Estonians. Similar cases of even more significant frequency change over a short geographic distance occur between the Southern Slavic speaking populations and their adjacent neighbors: namely Slovenians versus North Italians, and Macedonians versus Greeks.

This kind of 'peculiar' two-peak distribution pattern in Europe is uncharacteristic to other distinguished Y-chromosomal haplogroups and such a pattern is hard to explain by any possible migratory or expansion event. The explanation to such irregular distribution-pattern came with further studies, where due to new informative markers the improved resolution of phylogeny of hg I enabled to reveal distinct, clearly defined phylogeographical patterns of haplogroup I sub-clades.

Haplogroup I consists of several distinct sub-clades: I1a (defined by marker M253), I1b (defined by marker P37) and I1c (defined by marker M223), which jointly cover about 95% of hg I individuals. The rest 5% of individuals remain in I* clade (individuals who lack any known downstream markers inside haplogroup) and are distributed with extremely low frequency all over the spread area of the haplogroup. They may represent the real ancestral I* individuals and/or individuals, who belong to sub-clades, so far uncovered (Rootsi et al. 2004). Phylogenetic network of hg I STR haplotypes (Rootsi et al. 2004) points to characteristic haplotype patterns in different sub-clades that allow identifying possible founder haplotypes for the sub-clades. Sometimes (especially in case of typical haplotypes) certain haplotype motifs that are characteristic to specific sub-clade enable even to guess the possible affiliation to certain sub-clade (in case of lack of SNP typing).

The present distribution of different sub-clades of haplogroup I is considered to be connected to post-LGM re-colonization of Europe. After the end of LGM climatic improvement, repopulation of Europe started, most likely as expansions from isolated population nuclei from different refugial zones in Europe - Iberia (Franco-Cantabrian refugium), the present Ukraine (Periglacial) and from the northern Balkans (Dolukhanov 2000). The post-LGM expansion of haplogroup I sub-clades is prevailingly connected with expansions from Franco-Cantabrian and Balkan refugial areas.

Distribution map for Y-chromosome
haplogroup I



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