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GENETIC DIVERSITY IN FLEMISH Y-DNA

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Genetic Diversity in Flemish Y-DNA

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Abstract

More than a million Americans are descendants of Flemish immigrants. Close to 400,000 Flemish immigrants settled between Michigan and Oregon in the late 19th and early 20th centuries. Flemish people also had major influences on the English, the Scots, and the Irish.

Genetic genealogy is a relative young field that has made interesting discoveries regarding surname relationships. Surname relationships are, however, dependant on the origin of the surname, changes in spelling of surnames, interpretations and adaptations of surnames to new environments. In contrast, geographical DNA projects focus on a particular geographical area where people have experienced a common history over time. The interweaving of history, conventional, and genetic genealogy often produces a better picture of the evolution of a group of people. A first step in this direction is to discover the main haplogroups present in a particular population. This article focuses on refining the understanding of the distribution of haplogroups among people with Flemish roots, creating a baseline for the study of the mosaic of genetic diversity in Europe.

Introduction

The ancestors of the Flemish originally came from Flanders, a region located in what is today the northern part of Belgium. Flanders has an area of 5,221 square miles (13,522 square km), roughly the size of Connecticut. The current population of Flanders is slightly over 6 million, resulting in a population density of 886 per square mile (342 per square km).

The history of Flanders and of the Flemish people in particular provides an interesting background for the study of Flemish DNA that will lead to better understanding of the mosaic of European DNA. By interweaving history, genealogy, and genetic genealogy, part of this mosaic of Flemish DNA can be revealed.

This paper starts with a brief historical overview of Flanders and the Flemish people, and subsequently describes the datasets of Y-chromosome STR haplotypes assembled for the present study. Finally it provides the frequency distribution of the major haplogroups and discusses how this is different from previously published papers. The paper concludes by bringing together the origin of the main Y-chromosome haplogroups found in the Flemish, and discusses their European context. Portions of this article were previously published in "Flemish DNA & Ancestry" (Deboeck, 2007).

Historical Background

Centuries ago the deltas formed by three great rivers, the Weser, the Meuse, and the Scheldt, were inhabited by the Goths,¹ who were an ancient Teutonic people. These rivers deposited their muddy debris for ages on what became known as "the Low Countries." The fertility of these plains became fatal to the native possessors because many foreign tyrants sought to conquer these Low Countries. This aroused and inspired resistance among the inhabitants; they acquired the genius of liberty and of upholding independence. These natives, whose name became synonymous with *liberty*, were cultivators of soil; the tribe was called Frisii, Frisories or Frisians.

Some four hundred years after the fall of the Roman Empire, Charles the Bald, the first king of France, established the County of Flanders as a feudal fief. For five centuries Flanders remained independent of foreign policies and decisions. Thereafter, from the 13th till the

¹ According to the six century Gothic historian Jordanes, the Goths came from Sweden across the Baltic Sea to the basin of the Wisa (Vistula) river. By the third century CE they had migrated as far south as the lower Danube. According to their folklore the Goths once lived far north on the shores and islands of what is now Sweden. After long, slow wanderings through the forests of western Russia, the Goths reached the shores of the Black Sea. For a time the Goths ruled a great kingdom north of the Danube river. When in CE 375 the Huns swept into Europe from Asia, the Ostrogoths or East Goths were conquered and the Visigoths (the good Goths or noble Goths) had to seek refuge across the Danube within the boundaries of the Roman Empire. In 395 the Visigoths rose in rebellion and overran a large part of the Roman Empire. In 410 Rome itself fell into the hands of the Visigoths. The detailed history of the fights between Ostrogoths and Visigoths and their conquer of the Roman Empire can be found at <http://history-world.org/goths.htm>.

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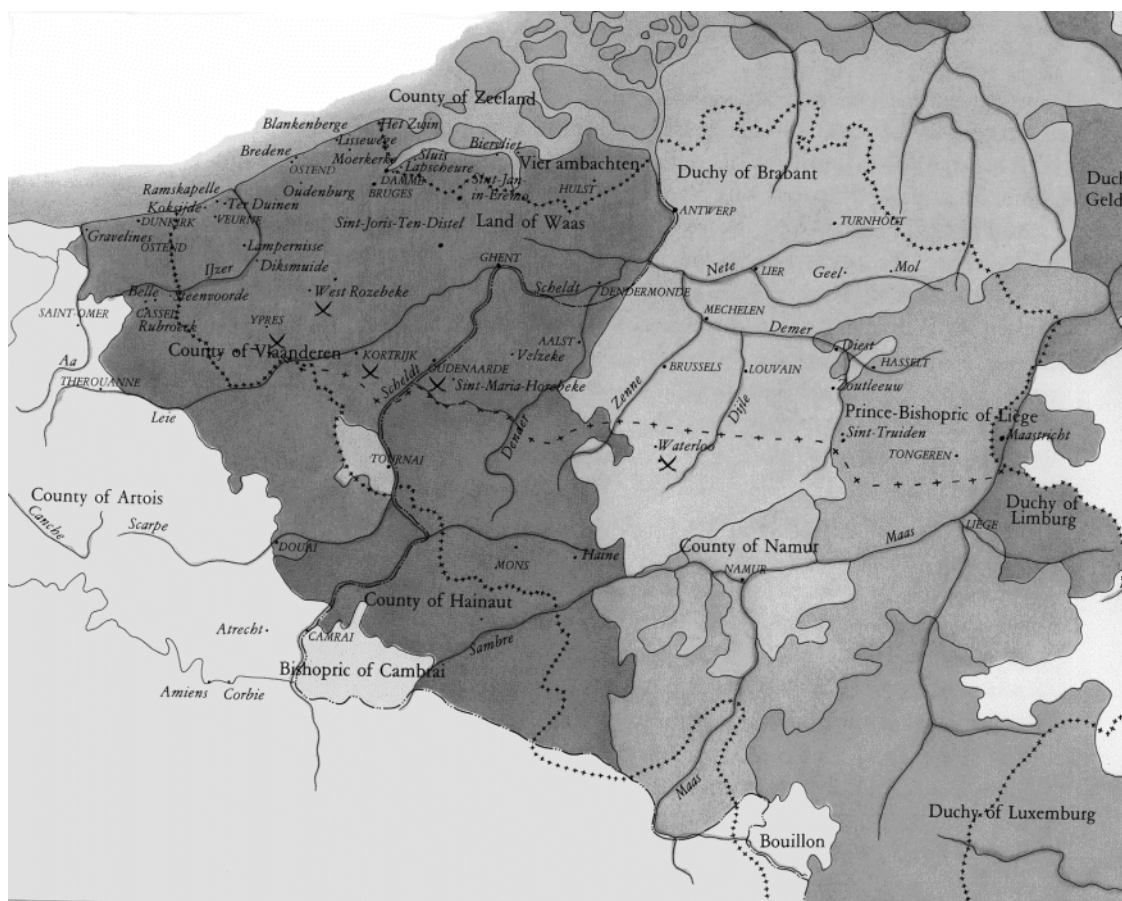


Figure 1 Map of the southern Low Countries in the late Middle Ages, including present-day Flanders (Source: Carson, 1990)

Table 1
Political History of Flanders

Political Status	Time Period
County of Flanders Established by First King of France	CE 862
Burgundian Netherlands	1384-1482
Habsburg Netherlands	1482-1556
Spanish Netherlands	1556-1713
Austrian Netherlands	1713-1789
United States of Belgium	1790
Austrian Netherlands	1790-1794
French Republic	1795-1804
French Empire	1804-1814
United Kingdom of Netherlands	1815-1830
Kingdom of Belgium (Unitary State)	1830-1993
Flanders: Federal Region/Community, Belgium	1993-Present

early part of the 19th century, the southern part of the Low Countries was occupied by foreign forces. Arnold Flemming wrote: "Happy is the land that has no history; no history, that is, of blood and strife. Such cannot be said of Flanders, it is full of history" (Flemming, 1930). The history of Flanders is a sequence of periods (see Table 1) in which Flanders was dominated by the Spanish, the Austrians, the French, and the Dutch, before it became a region or state of Belgium.

In 1830 the big powers of Europe created Belgium as an *artificial state* (other artificial states, which have fallen apart since their creation, were Yugoslavia and Czechoslovakia). Belgium was originally set up as a unitary state with a parliamentary system of government. Through four revisions of the constitution, the unitary state was transformed into an *ad hoc* federal state, with three regions responsible for territory-related matters and three communities responsible for personal matters. The complex socio-economic and political structures of the Belgium Federal Model² remain an "unfinished design."

² A description of the Belgian Federal Model may be seen as http://www.senate.be/english/federal_parliament_en.html.

Flanders now refers to that part of Belgium that is inhabited by speakers of Dutch or Flemish dialects, and the inhabitants are considered to be Flemish. A broader definition of “the Flemish” includes people who have Flemish roots, but have migrated to Britain, Canada, the U.S., or elsewhere. This broader definition was adopted in this study so that DNA samples collected from people living in the U.S. and elsewhere could be used and compared to DNA derived from sources in Flanders.

Methods

This study relies on the pooling of three sets of Y-chromosome STR data. The two larger datasets contain data on 12 Y-STR markers, DYS393, DYS390, DYS019, DYS391, DYS385a, DYS385b, DYS439, DYS389i, DYS392, DYS389ii, DYS437, and DYS438. The Flanders-Flemish DNA (FFDNA) project dataset has haplotypes with 12, 25, or 37 markers from Family Tree DNA’s (FTDNA’s) three panels of markers. Each set was collected in a different way from different subjects and is independent of the others.

The first set of Y-STR haplotypes was derived from the FFDNA project, launched by the author in November 2005. As of March 2007, 45 records had been submitted to this project at FTDNA. These records were mainly from people living in the U.S. who believed that their patrilineal lines came from Flanders. These initial 45 records were used for the first analysis undertaken in the spring of 2007 and published in September 2007 (Deboeck, 2007). Since September 2007, 18 more records have been added to the FFDNA project, bringing the total number of FFDNA samples to 63. While all of the participants who have joined the FFDNA project believe that their paternal lines come from Flanders, there is no way to verify this.

The map in Figure 2 is marked to indicate where members of the FFDNA project live. The map in Figure 3 shows the location of the most distant ancestors of those members. On the second map, three markers are shown in Ireland, but these are from people who believe that their ancestors migrated there from Flanders. Arnold Fleming wrote that “history is an eternal tangle of cross purposes, and we could not take a more complicated case than the heterogeneous factors lying behind the influence of the Flemings upon the British people” (Fleming, 1930).

In addition to the influence on Britain, Flemish emigration in the 19th and early 20th centuries has resulted in over one million people of Flemish descent currently living in the U.S. (Denys, 1984; Baye, 1987). These Flemish Americans clearly have Flemish ancestors (van Molle L., Pansaerts C, 1996). In sum, the maps and A. Fleming’s work show that in the U.S., England, Scotland, and Ireland there may be a lot of people who have ancestors who originally came from Flanders.

The second set of haplotypes is based on 112 DNA samples extracted from blood samples taken at the university hospital of the Catholic University of Leuven (KUL). According to Professor Ronny DeCorte, these blood samples were mostly taken from people who were from Leuven. Each of these 112 haplotypes contains 12 markers.

The modal values of the 12 markers for these 112 haplotypes correspond exactly with the modal values found in the 45 records collected via the FFDNA project. The fact that the modal values correspond so closely provides evidence that the data collected via the FFDNA project indeed represents DNA from people with Flemish roots.

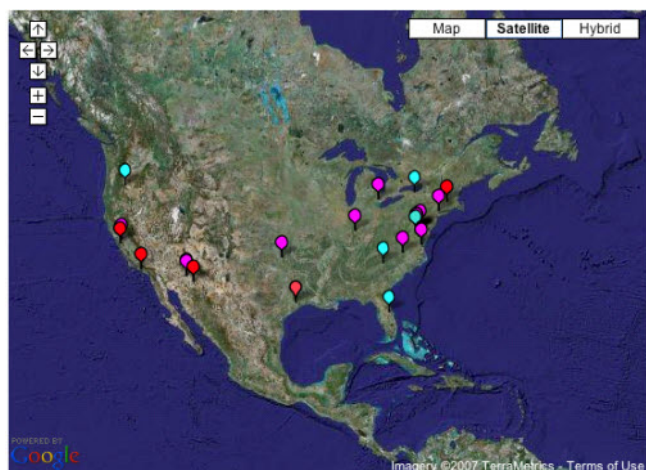


Figure 2 Residence locations of Flanders-Flemish DNA Project members.



Figure 3 Residence locations of the earliest known ancestors of Flanders-Flemish DNA Project members.

The third data set was derived from a genetic study of 113 unrelated Flemish males, who were typed for 12 Y-STRs. This dataset was obtained from G. Mertens and appeared in the Fall 2007 issue of this journal. The main result of that study showed that in this sample of 113 Flemings, there were 56.6% belonging to Haplogroup R1b, 19.5% belonging to Haplogroup I1 (I-M253), 8% to Haplogroup I2b2 (I-M223), 4.4% to Haplogroup E1b1b1 (E-M35, formerly E3b), and the remainder to Haplogroups G2a (G-M201), I2a (I-P37), J2a1b (J-M67), J2a1k (J-DYS445<7), J2b (J-M12) and L, ranging from 0.9 to 3.5% of the total (Mertens, 2007).

Merging all three data sets provided a total of 288 haplotypes with complete data for the ten markers DYS393, DYS390, DYS19, DYS391, DYS385a&b, DYS 439, DYS389-1&-2, and DYS392. This combined Flemish Y-STR dataset was then used to update the analyses previously carried out by Deboeck (2007) and Mertens (2007).

The methodology that was used consisted of the following steps:

1. All three data sets were merged into a single spreadsheet. The identifier and source of each haplotype was kept in a separate column.
2. The Haplogroup Predictor program (Atthey, 2005; Atthey, 2006) was used in batch mode to predict the haplogroups for the KUL-Leuven data set, and to reanalyze the haplogroup for the other two datasets so that all of the predictions would have the same basis. The 21-haplogroup version of the haplogroup program with northwest European prior probabilities was used.
3. The data records were sorted by source and haplogroup to compute the haplogroup frequencies for each data set.
4. The overall haplogroup frequencies were calculated for the combined dataset.
5. The allele frequencies were calculated for each marker in the combined dataset for Haplogroups R1b and I1.
6. The modal haplotypes for the most prevalent haplogroups in the combined Flemish dataset were determined.
7. For each of the most prevalent haplogroups, the difference in origin and history of the haplogroups were compared.

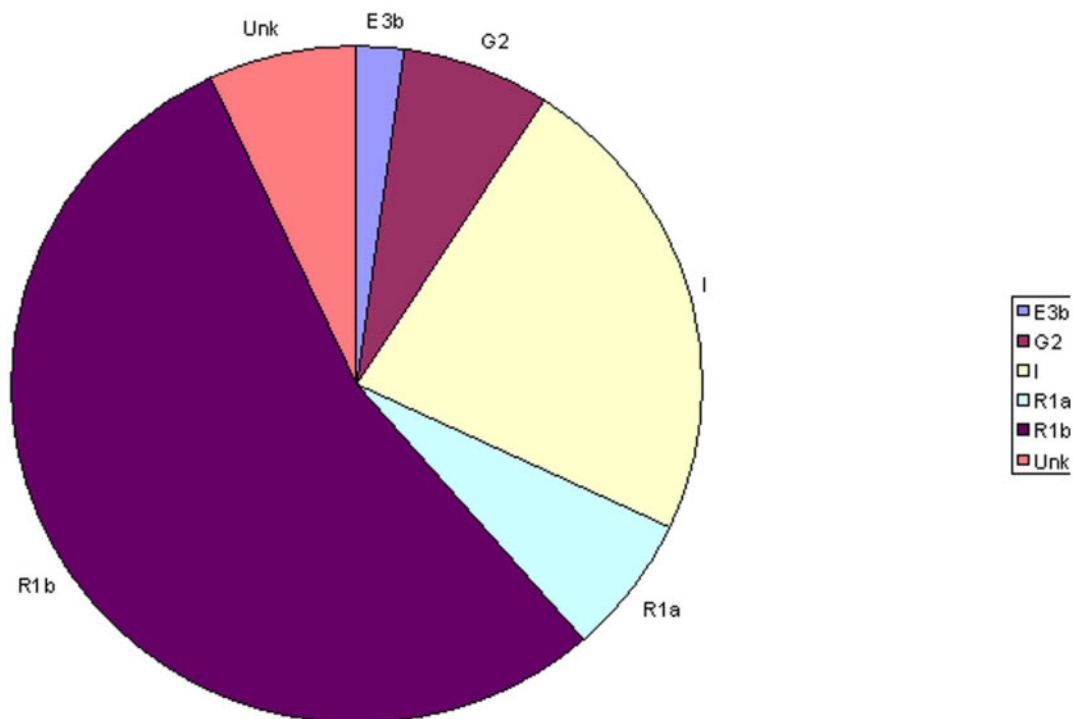


Figure 4 Distribution of haplogroups in the original (2007) FFDNA project analysis. In this chart the names of the haplogroups are those that were in use at that time (ISOGG, 2007).

Table 2
Flemish R1b Modal Haplotype (FMH) with Allele Frequency Distributions About the Modal

[illegible]

Table 3
Flemish I1 Modal Haplotype with Allele Frequency Distributions About the Modal Values

[illegible]

Table 4
Distribution of Haplogroups in the Samples Assembled for this Study

Original FFDNA (Published Fall 2007)				KUL Data (Original Analysis 2007)				Mertens Study (JOGG, Fall 2007 Issue)				Flemish Pooled Data (ISOOG-2008 Names)				Grouped By Major Haplogroup			
Haplo- group	No. of Haplo- types	Percent of Total		Haplo- group	No. of Haplo- types	Percent of Total		Haplo- group	No. of Haplo- types	Percent of Total		Haplo- group	No. of Haplo- types	Percent of Total		Haplo- group	No. of Haplo- types	Percent of To- tal	
				E3a	2	1.8%						E1b1a	2	0.7%		E1b1a	2	0.7%	
E3b	1	2%		E3b	5	4.5%		E3b	5	4.4%		E1b1b	12	4.2%		E1b1b	12	4.5%	
G2	3	7%		G2	2	1.8%		G2	4	3.5%		G2a	10	3.5%		G	10	3.5%	
				G5	0							G2c	0						
I	10	23%		H	0							H	0						
				I1a	13	11.5%		I1a	22	19.5%		I1	45	15.3%		I1	45	15.3%	
				I1b1 x I1b1b	1	0.9%		I1b1	1	0.9%		I2a x I2a2	4	1.4%		I2a	6	2.1%	
				I1b1b	1	0.9%						I2a2	2	0.7%					
				I1b2 x I1b2a	1	0.9%						I2b x I2b1	2	0.7%		I2b	15	5.2%	
				I1b2a	1	0.9%		I1b2a	9	8.0%		I2b1	13	4.5%					
				J1	1	0.9%						J1	2	0.7%		J1	2	0.7%	
				J2a1b	2	1.8%		J2a1b	2	1.8%		J2a1b	4	1.4%					
				J2a1k	4	3.6%		J2a1k	3	2.7%		J2a1h	7	2.4%					
				J2a1 x J2a1b/h	3	2.7%						J2a1 x J2a1b/h	2	0.7%		J2	15	5.2%	
				J2b	0			J2b	2	1.8%		J2b	2	0.7%					
				L	0			L	1	0.9%		L	1	0.3%		L	1	0.3%	
				N	0			N				N	0						
				Q	0			Q				Q	1	0.3%		Q	1	0.3%	
R1a	3	7%		R1a	9	8.0%		R1a				R1a	12	4.2%		R1a	12	4.2%	
R1b	24	54%		R1b	68	60.2%		R1b	64	56.6%		R1b	166	57.6%		R1b	166	57.4%	
				K2	0							T	0			T			
Unkn	3	7%		Unkn								Unkn	1	0.3%		Unkn	1	0.3%	
Total	45			Total	112			Total	113			Total	288			Total	288		

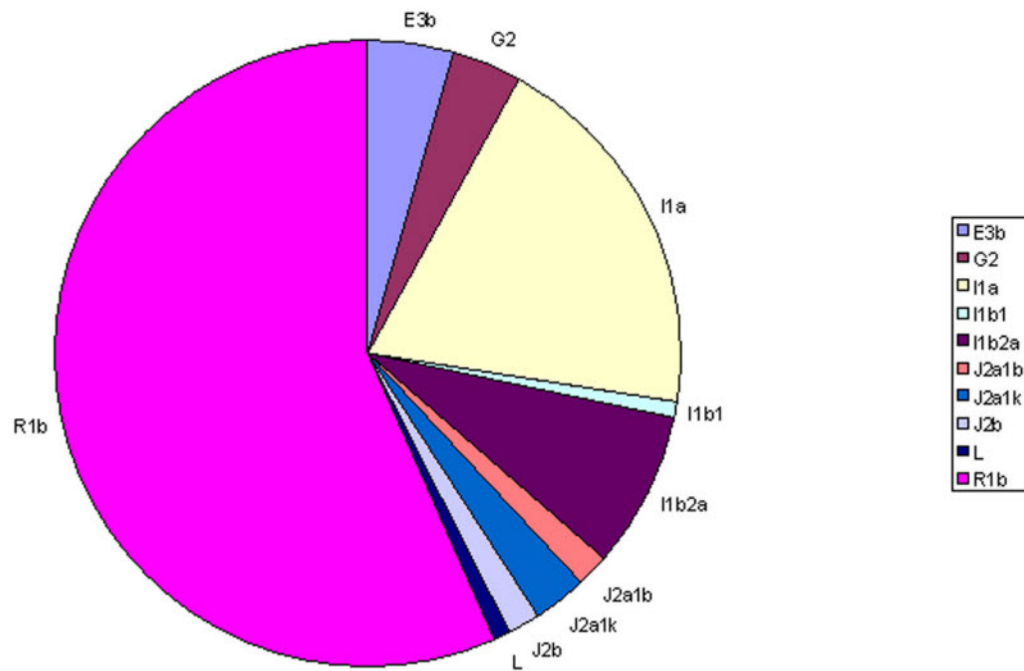


Figure 5 Distribution of Y haplogroups from the Mertens study. This study used the ISOOG-2007 haplogroup names.

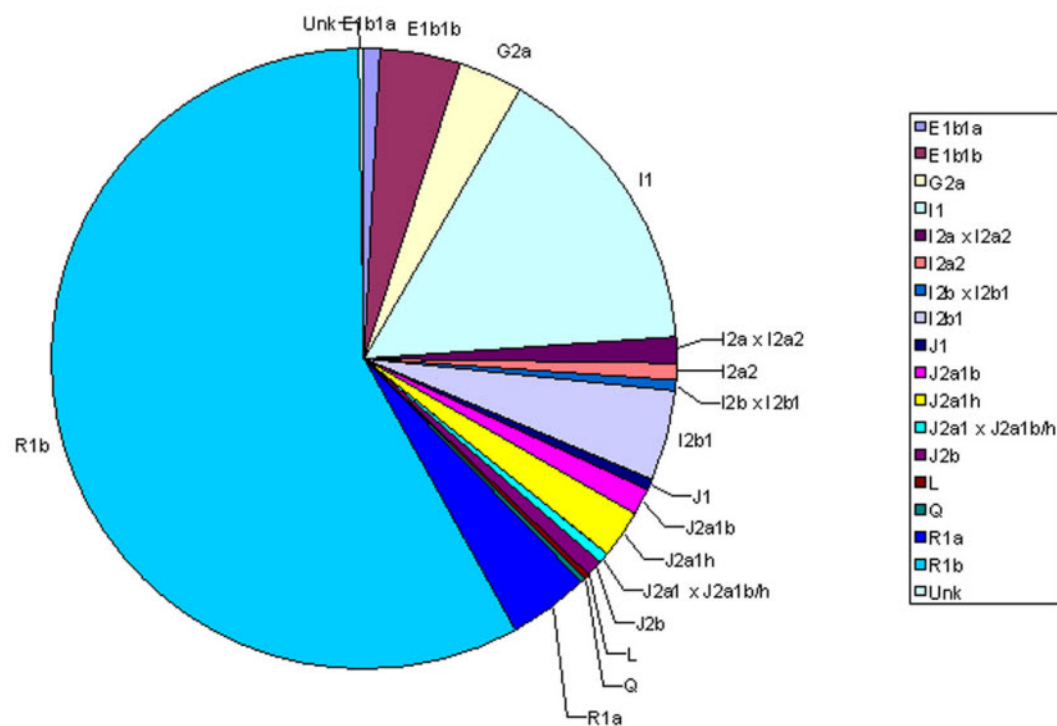


Figure 6 Distribution of Y haplogroups from the pooled Flemish data. In this chart, the current ISOOG-2008 haplogroup names are used.

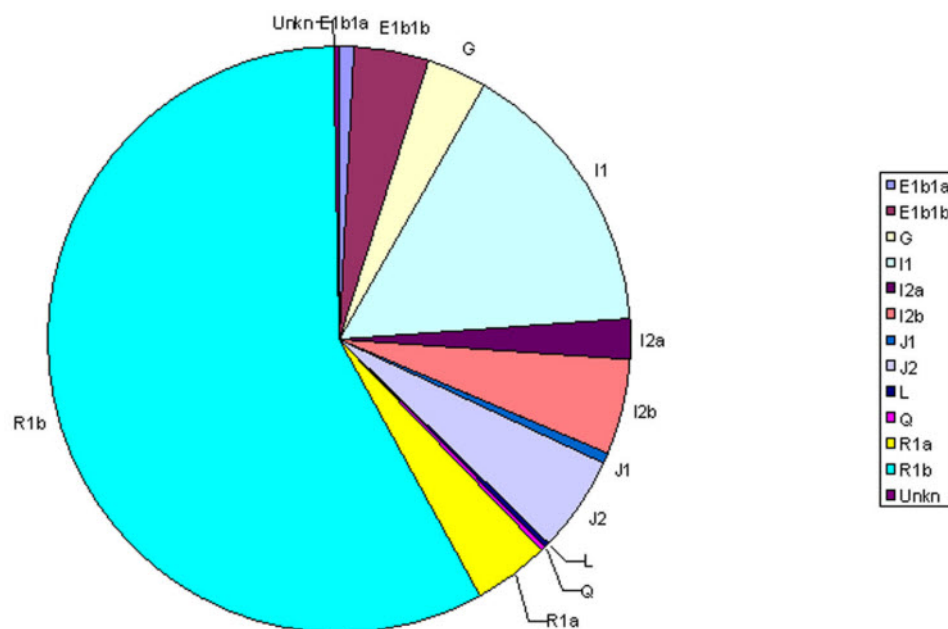


Figure 7 Distribution of major Y haplogroups from the pooled Flemish data. In this chart the ISOGG-2008 haplogroup names were used.

Results

The main results from applying the above steps produced a table of allele frequencies for 37 markers in 166 Flemish R1b haplotypes and 45 I1 haplotypes as shown in Tables 2 and 3; Table 4 shows the haplogroup distributions from the three datasets, both separately and combined; a series of pie charts in Figures 4-7 show the distribution of haplogroups in these datasets; and Table 5 compares the Flemish modal haplotypes with the modal haplotypes of the most common haplogroups.

Table 2 shows the allele frequency distributions for Flemish members of Haplogroup R1b, while Table 3 presents similar data from Haplogroup I1. However, note that for some markers there is insufficient data for an accurate calculation of the allele frequencies or even the modal value--these are subject to change as more data is accumulated. Table 4 provides the haplogroup distributions for the pooled Flemish haplotypes.

A comparison of Figures 4 and 5 shows that the data obtained via the FFDNA project corresponds closely to the 113 records used by G. Mertens in a study of paternity cases in Belgium. The dominant haplogroup in both cases was R1b, which represents between 54% and 56.6% of the total. The second largest haplogroup in these two samples is Haplogroup I1 which represents between 19.5% and 25% of the total. Other haplogroups that occur are E1b1b, representing between 2% and 4.4%, and Haplogroup G2a, representing between

3.5% and 7% of the population. A difference between the FFDNA sample and the Mertens dataset is in the occurrence of Haplogroup R1a, which represents 7% in the first sample and does not appear in the second, though if the true frequency is only 1-2%, this is not a surprising result.

Figure 6 provides the detailed distribution of haplogroups found among the 289 Flemish haplotypes. The haplotypes from all three data sets were submitted to the 2008 21-haplogroup version of Whit Athey's Haplogroup Predictor program (Athey, 2005, 2006) so that all of the predictions would have the same basis. This produced a number of changes from their old designations, some of which simply involve newer nomenclature (ISOGG, 2008); these changes are reflected in Table 4, which was used to produce Figure 6.

Combining the subhaplogroups' frequencies into the major haplogroups produces the distribution shown in Figure 7 and allows direct comparison with the G. Mertens results. An analysis of the full set of 288 haplotypes shows that 57.6% are Haplogroup R1b, 15.3% are I1 (old I1a), 5.2% are J2, 4.5% are E1b1b (old E3b), 4.2% are R1a, and 3.5% are G.

Table 5 compares the Flemish (R1b) Modal Haplotype (FMH) with the modal haplotypes of other R1b groups. Where the allele value of a particular marker in the FMH differs from the allele value of the other modal haplotypes, the values are shown in red font. This

comparison shows that the FMH differs on only three markers from the Atlantic Modal Haplotype (AMH). On DYS449 the FMH has a value of 30 while the AMH has 29; on DYS456 the FMH has a value of 16 while the AMH has 15, and on CDYa the FMH has a value of 36 while the AMH has 37. It should be noted that for CDYa, there is very little difference in the FMH allele frequency for a value of 36 versus 37.

A comparison of the FMH with the modal haplotype of the Frisian R1b cluster of McEwan (2006) shows differences on the markers DYS390, DYS447, DYS449, GATA-H4, DYS456, DYS576, and CDYa/b, plus differences in the complex marker, DYS464.

Other comparisons: a comparison of the FMH with the R1b modal values from the German geographic project at FTDNA shows that they differ on only one marker, DYS449. A comparison of the FMH with the R1b modal values from the Spanish geographic project at FTDNA shows that they differ on five markers, DYS439, DYS458, DYS464d, GATA-H4, and DYS456. A comparison with the R1b modal from the British Isles geographic project at FTDNA shows that the FMH differs on three markers with the British Isles R1b modal (DYS 449, CDYa, and CDYb. In summary there are some differences between the FMH and other major R1b population groups in Europe, which invites further investigation.

Table 6 shows a similar comparison for the Flemish I1 modal haplotype. The modal values for many of the markers are based on fewer than 10 haplotypes, so no firm conclusions may be drawn for these markers. However, one notable difference with the Frisian I1 modal haplotype (McEwan, 2006) is on DYS390, where adequate data exist. The Flemish I1 modal haplotype has a value of 24 on this marker, matching the overall European I1 modal haplotype in this case, while the Frisian I1 modal haplotype has a value of 23.

Discussion

What are the main differences between the haplogroups that are most prevalent among the Flemish?

Spencer Wells' book, *Deep Ancestry*, describes the haplogroups as follows:

- Haplogroup R1b members are descendants of someone who 30,000 years ago gave rise to the defining marker M343. These descendants that dominated the human expansion into Europe are likely the same as the *Cro-Magnons* (Wells, 2007, p 226).
- Members of Haplogroup I1 have the defining genetic marker M253, and moved 15,000 years ago from their refugia in the Balkans to the

north of Europe. This haplogroup is still very common in Scandinavia and hence it is likely that many Vikings descended from this line. The Viking raids on the Low Countries and Britain help to explain the dispersal of this lineage (Wells, 2007, p 213-14).

- Haplogroup E1b1b, characterized by the M35 marker, appeared in the Middle East among populations of the first farmers who spread agriculture from the Middle East to Europe (Wells, p209).
- Haplogroup G2a (referred to as G2 in the book), identified by the marker P15, arose in the Middle East and spread westwards through modern Turkey into southeast Europe. Most migrations took place more than 15,000 years ago before much of Europe was locked in ice during the last glacial maximum. When the glaciers finally began to recede, the G2a lineage expanded northward and eastward to repopulate Europe (Wells, 2007, p 211).

It should be noted that almost all haplotypes classed as R1b in this geographic study are likely also to be R1b1b2-M269. Most of the present-day European males with the M343 marker also have the P25 and M269 markers. These markers define the R1b1b2 subclade (ISOGG, 2008). The subclade R1b1b2g (defined by S21/U106), although recently discovered, appears to be the most common downstream marker from R1b1b2, appearing in over 35% of those R1b1b2 people tested. This group has a maximum in Frisia (the Netherlands) and, in general, is the predominant R1b sub-haplogroup in northwest Europe. It is also found in Belgium, in the UK, in southern Sweden, Switzerland, and Italy. It only sporadically appears in Spain, Poland and Lithuania (Polish), Finland (Swedish) and Romania (Romanian). The S21/U106 subclade may have originated near the end of the last ice age as Europe began to be repopulated, or perhaps more or less 9000 years before the present, possibly in the northern European mainland.

In summary, the analysis of three datasets of Flemish Y-STR values, collected from three independent sources, confirm the dominant presence of Haplogroup R1b in Flanders. In addition, Haplogroup I1-M253, and to a smaller extent Haplogroups I2b1-M223, J2, E1b1b, R1a, G2a, and I2a, have been shown to occur among Flemish people. The data collected via the FFDNA project, which was mainly submitted by people living in the USA, is fairly representative of the overall distribution of Flemish DNA. Hence there is continuity in the paternal lines of the Flemish and Flemish-Americans. The genetic characteristics of a small population living in the north of Europe provide a glimpse into the complexity of the genetic mosaic in Europe.

Table 5
Flemish R1b1b Modal Values Compared to Other European R1b1b Groups

	393	390	019	391	385a	385b	426	388	439	389i	392	389b	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCAa	YCAB	456	607	576	570	CDYa	CDYb	442	438
Flemish (R1b) Modal Haplotype	13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	30	15	15	17	17	11	11	19	23	16	15	18	17	36	38	12	12
Atlantic Modal Hap- lotype	13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	15	18	17	37	38	12	12	
Frisian (R1b) Modal Haplotype	13	23	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	24	15	19	29	15	16	17	18	11	10	19	23	17	15	17	37	39	12	12	
German (R1b) Mod- al Haplotype	13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	15	18	17	36	38	12	12
Spanish (R1b) Mod- al Haplotype	13	24	14	11	11	14	12	12	11	13	13	16	18	9	10	11	11	25	15	19	30	15	15	16	17	11	10	19	23	15	18	17	36	38	12	12	
British Isles (R1n) Modal Haplotype	13	24	14	11	11	14	12	12	12	13	13	16	17	9	10	11	11	25	15	19	29	15	15	17	17	11	11	19	23	16	15	18	17	37	39	12	12

Table 6
Flemish I1 Modal Values Compared to Other European I1 Groups

	393	390	019	391	385a	385b	426	388	439	389i	392	389b	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	460	H4	YCAa	YCAB	456	607	576	570	CDYa	CDYb	442	438
Flemish (R1b) Modal Haplotype	13	22	14	10	13	14	11	14	11	12	11	16	15	8	9	8	11	22	16	20	28/29	12	14	15	16	10/11	10	19	21	14	14	16/17	19	34	36	12	10
I1 Modal	13	22	14	10	13	14	11	14	11	12	11	16	15	8	9	8	11	23	16	20	28/29	12	14	15	16	10	10	19	21	14	14	16	19	35	37	12	10
Nordtvedt I1 "Norse"	13	23	14	10	14	14	11	14	11	12	11	16	15	8	9	8	11	23	16	20	28/29	12	14	15	16	10	10	19	21	14	14	16	19	35	37	12	10
Sweden I1 Modal Haplotype (Karlsson (2006))	13	23	14	10	14	14	11	14	11	12	11	16	15	8	9	8	11	23	16	20	28/29	12	14	15	16	10	10	19	21	14	14	16	19	35	37	12	10
Germany Project I1 Modal Haplotype	13	22	14	10	13	14	11	14	11	12	11	16	15	8	9	8	11	23	16	20	28/29	12	14	15	16	10	10	19	21	14	14	16/17	20	35	37	12	10
British Isles Project I1 Modal Haplotype	13	22	14	10	13	14	11	14	11	12	11	16	15	8	9	8	11	23	16	20	28/29	12	14	15	16	10	10	19	21	14	14	16/17	19	35	37	12	10

Future research should concentrate on drawing more in-depth comparisons of Flemish DNA with the patterns observed in Frisian, German, British, Spanish and French populations. Based on the history of Flanders it is reasonable to assume that the German influence on Flemish DNA is likely to be much stronger than, say, the French. The British influence on Flemish DNA is likely to be minimal since Britain was never an occupying power in Flanders. However Flemish DNA may be found back on the British Isles since centuries ago there were large migrations of Flemish people to England, Scotland, and Ireland. This should stimulate genetic genealogists interested in the British Isles to trace their ancestry to the continent, in particular to Flanders, that small piece of land across the Channel that has been a battleground for centuries and continues to be the center of attention as to its influence on the political unity of Europe.

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Web Resources

<http://www.hprg.com/hapest5/>
Haplogroup Predictor Program

<http://www.familytreedna.com/public/Flanders/>
Flanders-Flemish DNA Project web site

http://www.senate.be/english/federal_parliament_en.html
Belgian Federal Model

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