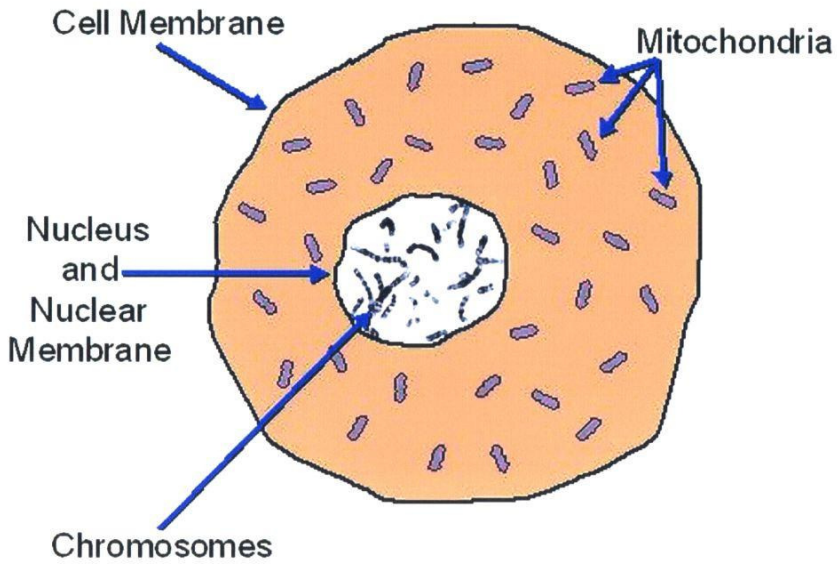
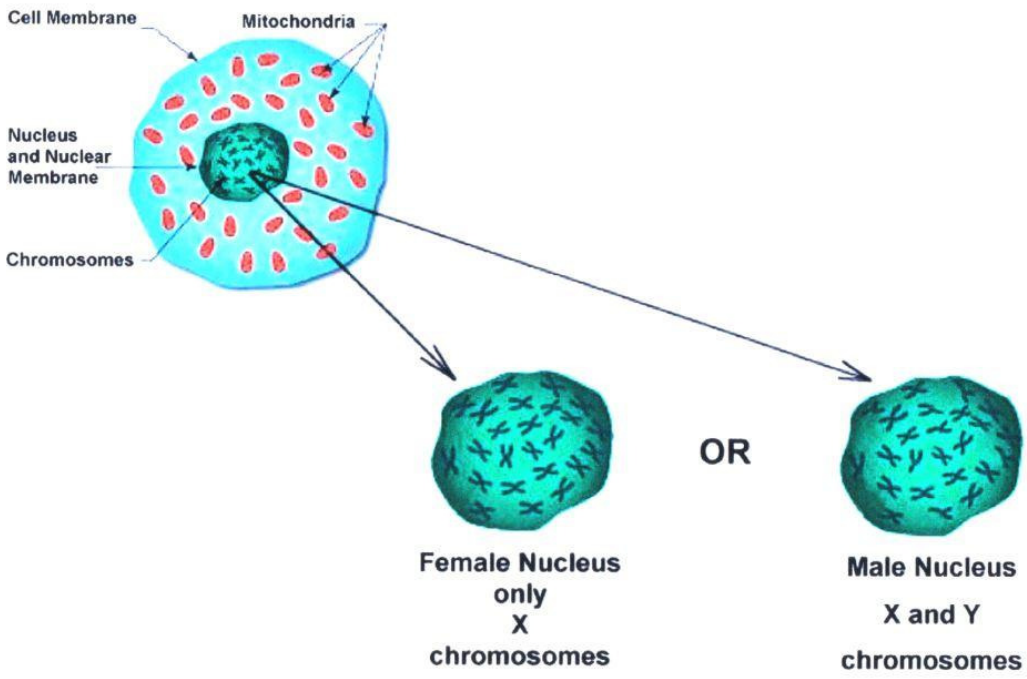
Introduction to Genetic Genealogy

Every human cell (except red blood cells and sperm and eggs) has an identical set of 23 pairs of chromosomes which carry all the hereditary information that is passed from parent to offspring. These chromosomes are located in the nucleus of each cell.

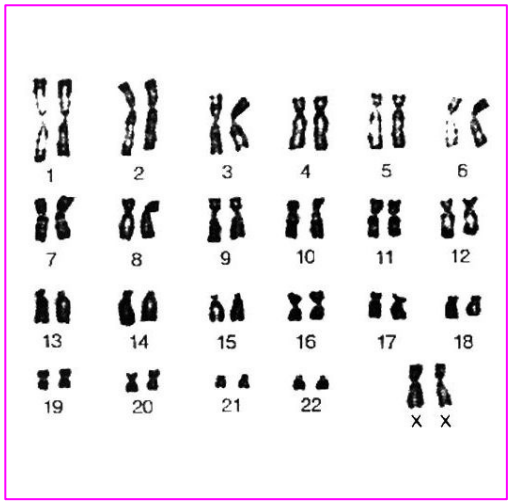


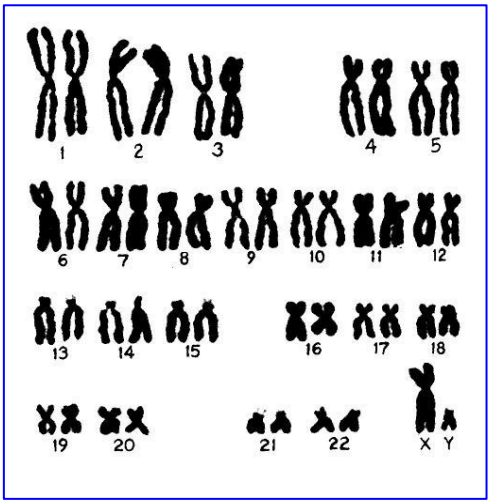
Human Cell

The partners of 22 pairs are matched in size, shape, and function in both males and females. In females, the 23rd pair, called the X chromosomes, is also matched. However, in males, the 23rd pair of chromosomes is mismatched with one X chromosome (received from the mother) and one Y chromosome (received from the father).



Female Nucleus and Male Nucleus





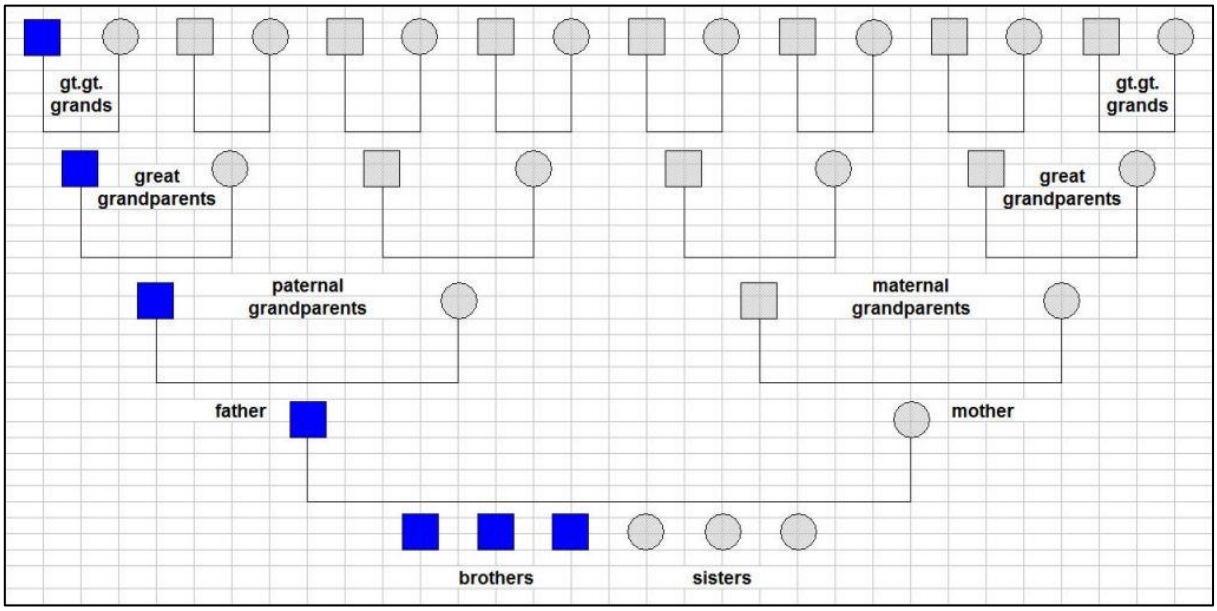
Female Chromosomes

23rd Pair = XX

Male Chromosomes

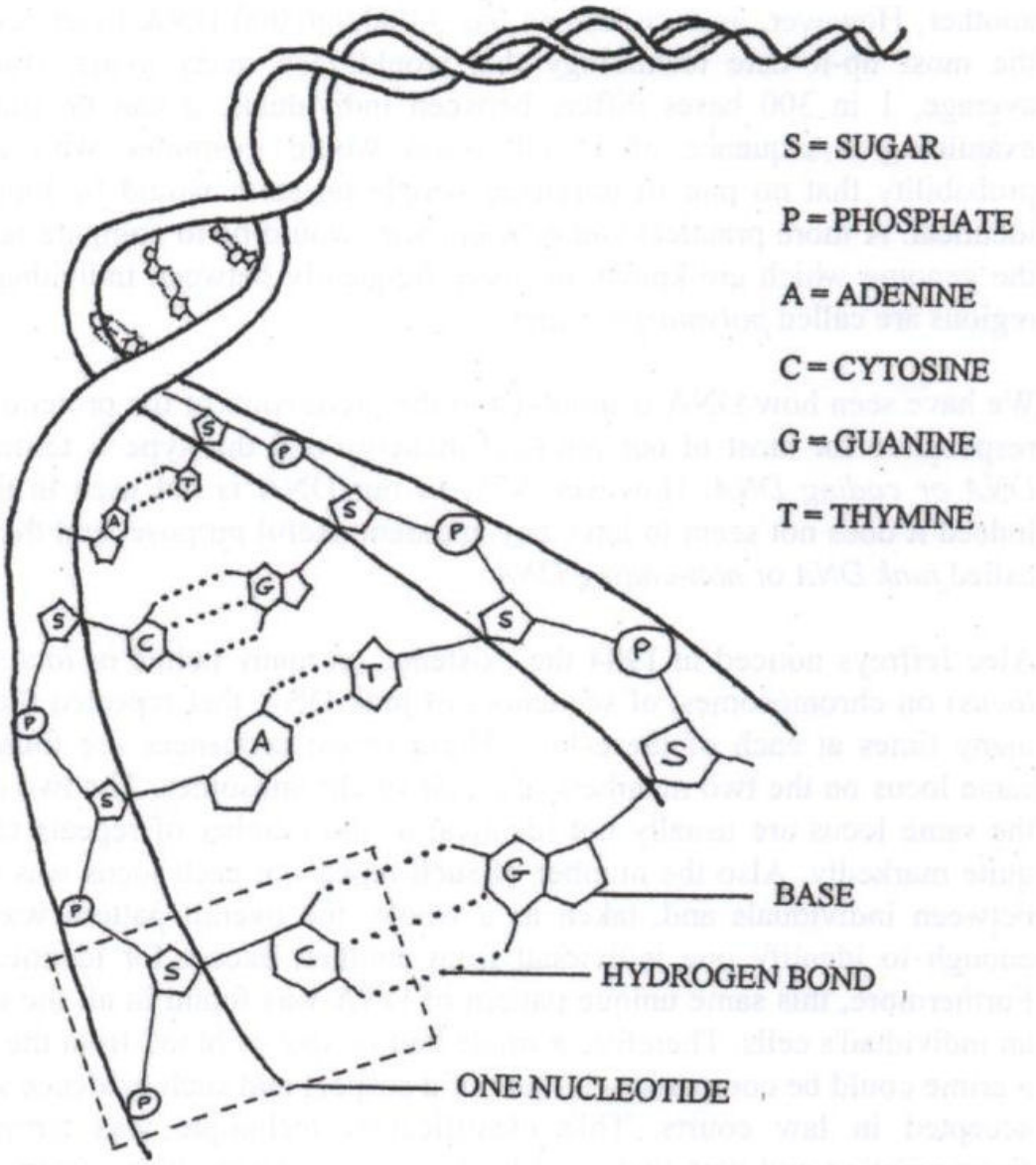
23rd Pair = XY

Whereas all of the other chromosomes are blended, shuffled and distributed randomly when sex cells (egg and sperm) are formed, **the Y chromosome is always handed down virtually intact from father to son. For this reason, all of the direct male descendants of one male will share identical or nearly identical Y chromosomes.**



Inheritance of Y Chromosome through Paternal Descent

Each chromosome, including the Y chromosome, is a long strand of DNA (deoxyribonucleic acid). The DNA molecule is a chain made of four different subunits which are conveniently referred to as G, A, T and C (guanine, adenine, thymine and cytosine). The order of the four subunits in about 30,000 segments of human DNA, called genes, provides codes for all of a person's traits such as height, eye colour etc.



DNA (deoxyribonucleic acid)

In between these coding sections (genes) are long stretches of DNA that serve no known function. Many segments of this so-called “junk” DNA contain short repeating patterns (motifs) of the subunits. For example, the series TACTACTAC is a repeat of 3 sets of the pattern TAC. **These repeating patterns are called STRs (short tandem repeats).**

The same patterns occur in the same locations in everyone's chromosomes. However, the number of sets (repeats) varies from person to person. Since the Y chromosome is passed nearly unchanged from father to son, all descendants of the same man will share the same number of repeats at the same locations (loci) on their Y chromosomes. **Taken together, the repeat numbers for a set of Y chromosome loci is a biochemical signature for all the male-line descendants of a given male.** That signature can be used to identify his descendants even if surnames are changed along the way.

Only rarely does a mutation occur between a father and son causing one (or rarely more) STR to gain or lose one (or rarely more) pattern set. Over many generations, changes accumulate. These variations allow us to identify different lineages and provide evidence for genealogical relationships when fortuitous mutations define branching points in descendants of a common ancestor.

The locations for which repeats are counted are called markers. Most markers on the Y chromosome are called DYS markers (DNA Y chromosome segment markers). Individual markers are designated by a number or a combination of a number and letter**. A list of the values (number of repeats) for all of one man's markers is called his Haplotype.**

The Flannery Clan Y-DNA Project uses the Y37 test. This test checks the number of repeats at 37 markers, and provides a string of 37 numbers like a combination code. Genetic relationships can be checked by comparing codes: the better the match, the closer the relationship.

DYS#	393	390	394	391	385a	385b	426	388	439	389i	392	389ii
repeats	13	24	14	10	11	14	12	12	12	14	13	30

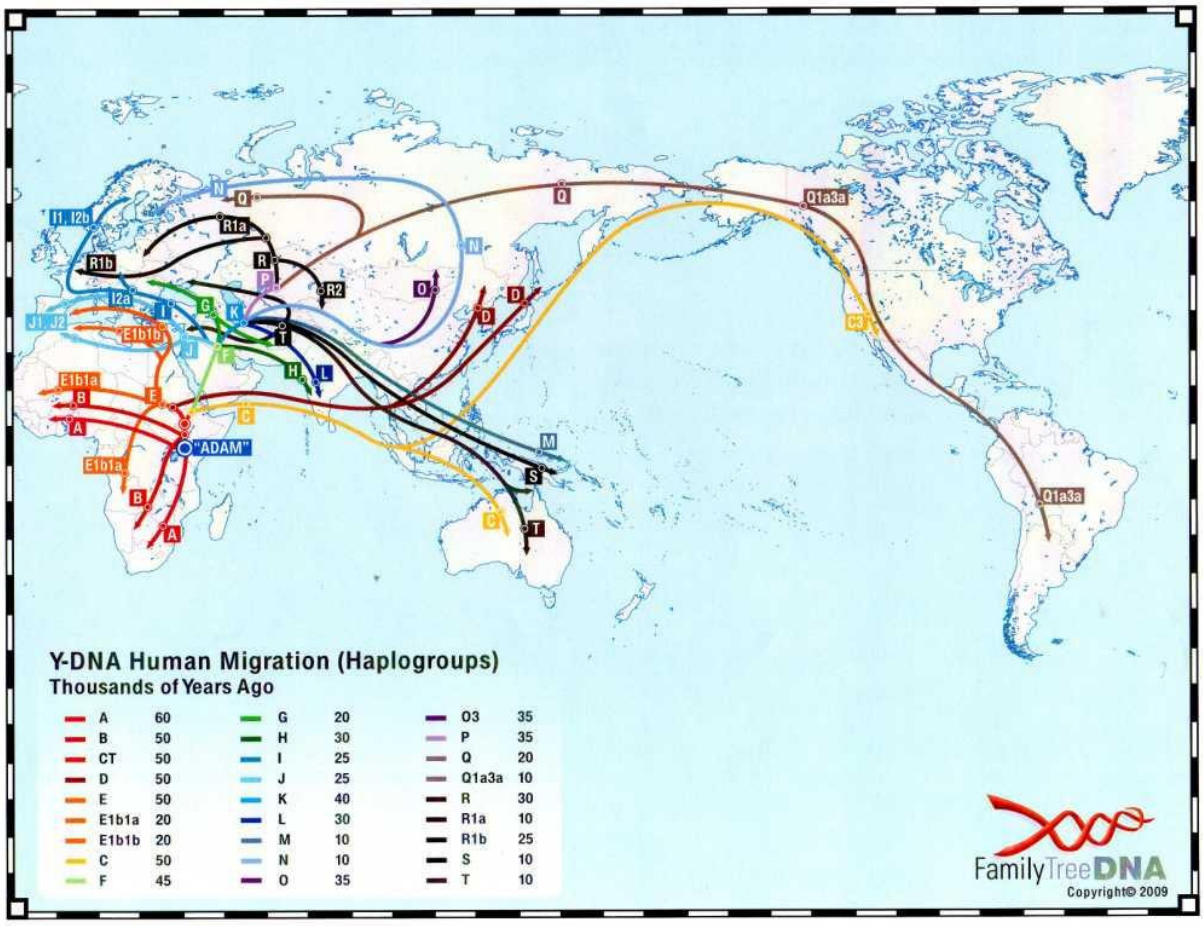
458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
16	9	10	11	11	26	16	19	29	15	15	17	17

460	GATAH4	YCAIIa	YCAIIb	456	607	576	570	CDYa	CDYb	442	438
11	11	19	23	16	15	18	17	38	38	12	12

37-marker Haplotype for a typical Munster Flannery

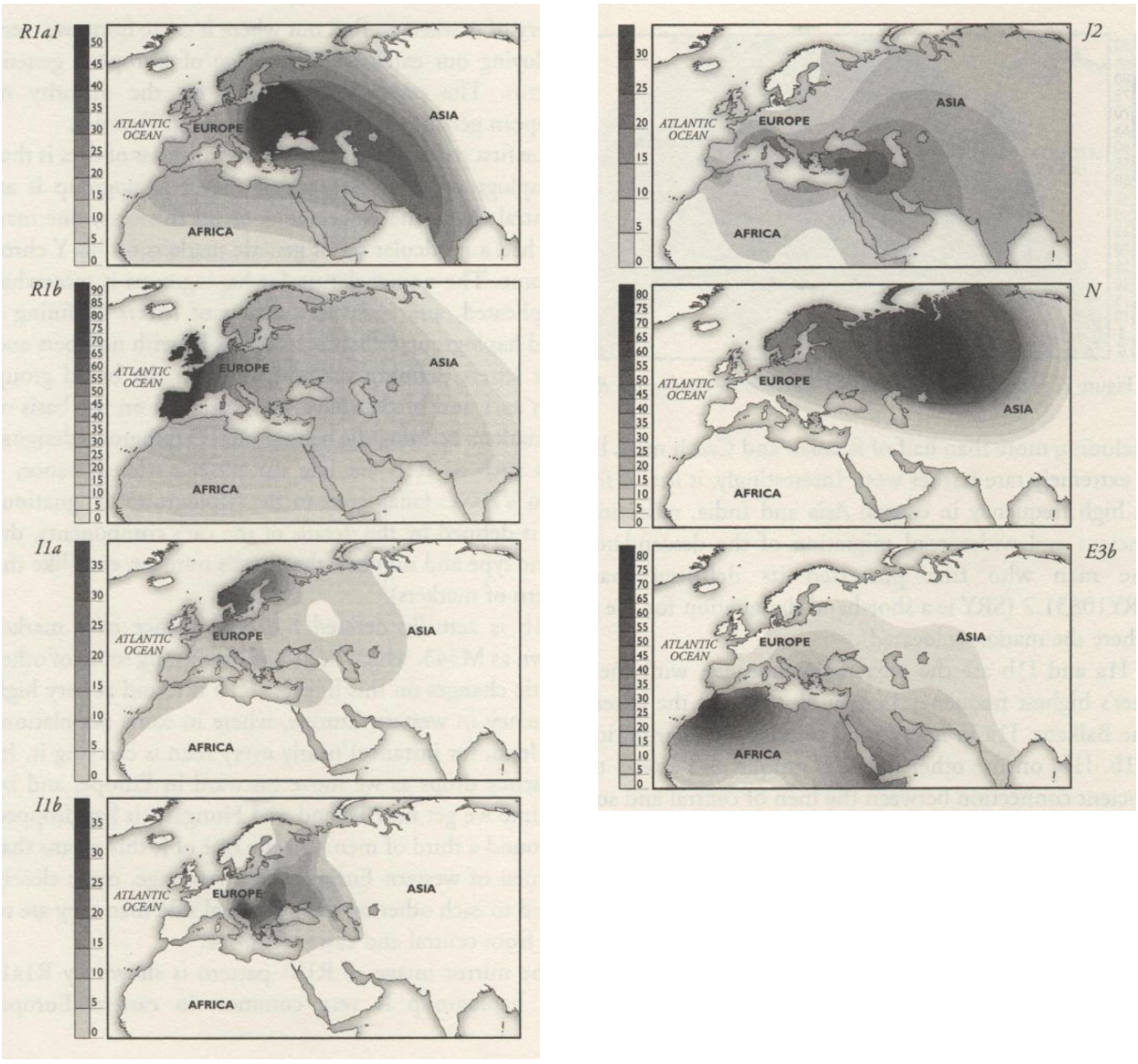
In addition to being characterised by its array of STR marker repeats, Y chromosomal DNA, like the DNA of the other chromosomes, can also be characterised by a second kind of mutation which involves the **substitution of one of the subunits for another**. These mutations are called **SNPs (single nucleotide polymorphisms)**.

SNP mutations are rare. In fact, they occur so rarely that they are considered unique events in human history – each one occurring only once in only one person. **A Y chromosome haplogroup is defined as all the male descendants of the one person in which a specific Y chromosome SNP first appeared.** They will, of course, all test positive for this mutation. The Y Chromosome Consortium has defined 20 major haplogroups designated by the letters A to T which effectively define the races of mankind.



Geographical Spread of Haplogroups A to T

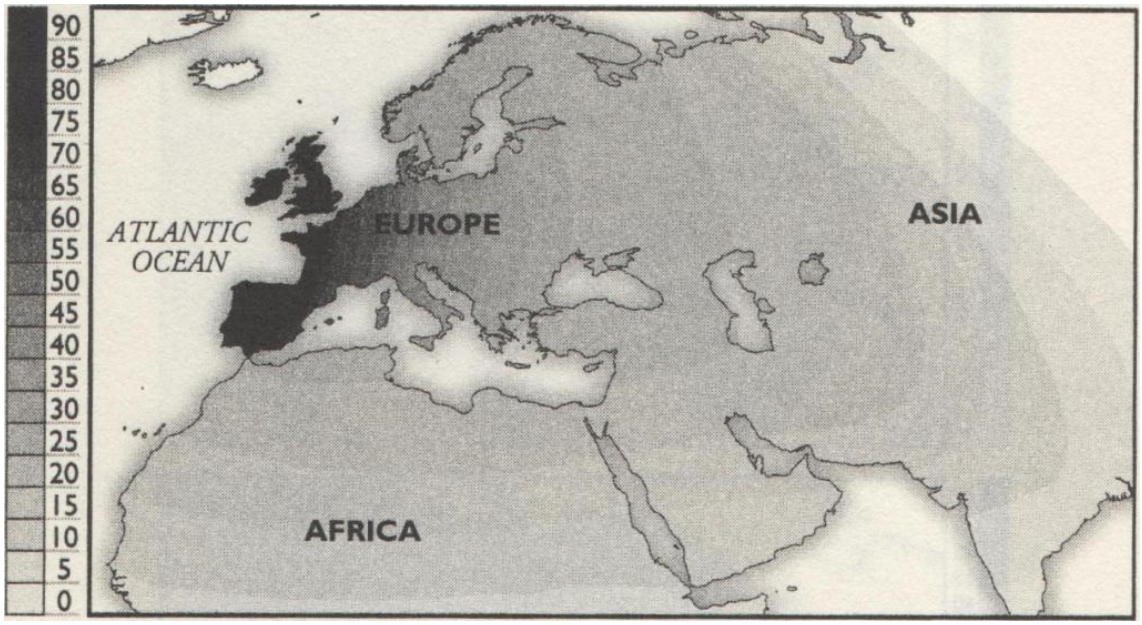
Subgroups are identified by additional SNPs which have occurred later in individual lines. They have been given numeric names which follow the haplogroup name. Additional branches are designated by lower case letters. Seven of these haplogroups (R1a1, R1b, I1a, I1b, J2, N and E3b) account for more than 95% of the haplogroups found in European populations.



Distribution of the 7 Major Haplogroups in Europe

R1b is found at very high frequency in western Europe, especially in the west of Ireland. R1a1 is very common in eastern Europe. I1a has high frequency in Scandinavia. I1b is common in the Balkans. J2 has high frequency in the fertile crescent of the Middle East. E3b is common in Greece. N occurs most frequently in northern Scandinavia and eastern Europe.

This is relevant to our study because the haplogroup R1b carried by the majority of indigenous Irish is easily differentiated from haplogroup I1a shared by the Vikings of Norway and Denmark and their Norman descendants.



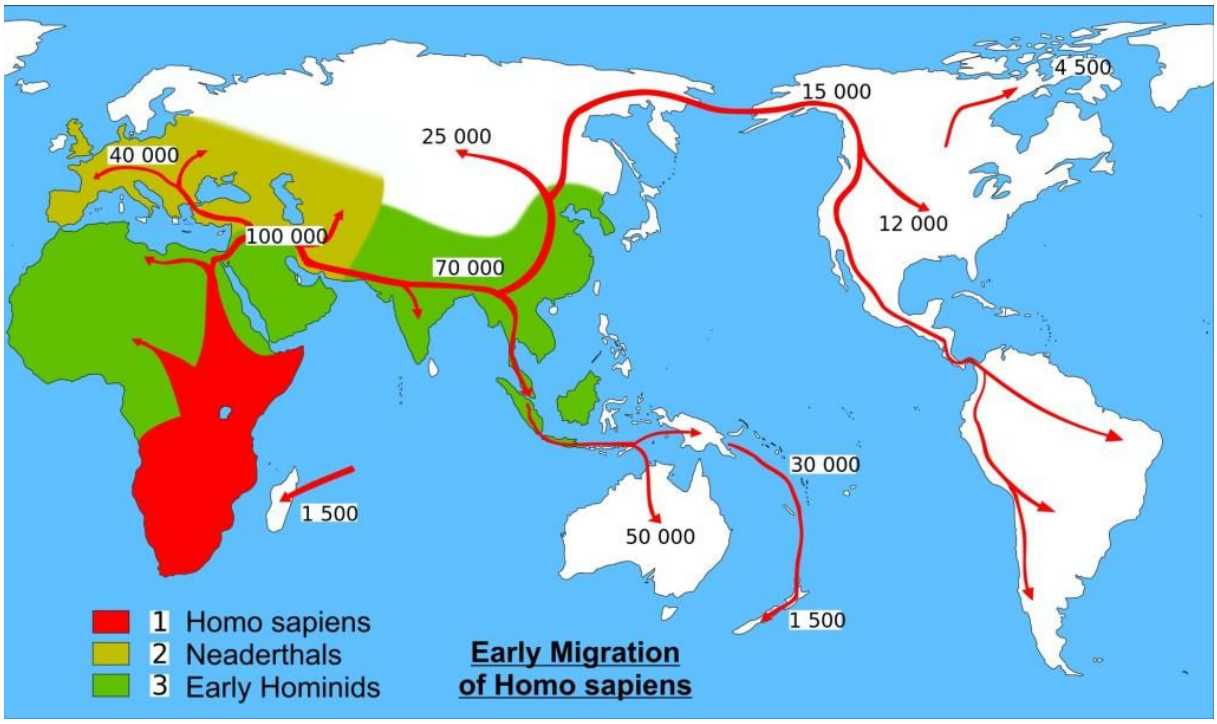
Distribution of Haplogroup R1b

FamilyTreeDNA and other commercial laboratories do offer SNP testing for determination of haplogroups. So far, only STR markers have been evaluated in the Flannery Clan Y-DNA Project. However, it is usually possible to estimate a person's haplogroup based on the pattern of his STR markers.

Of great interest are current projects using data from SNP and STR analyses to map the paths of human migration out of Africa and through the rest of the world. The migration through Europe is where our study must begin.

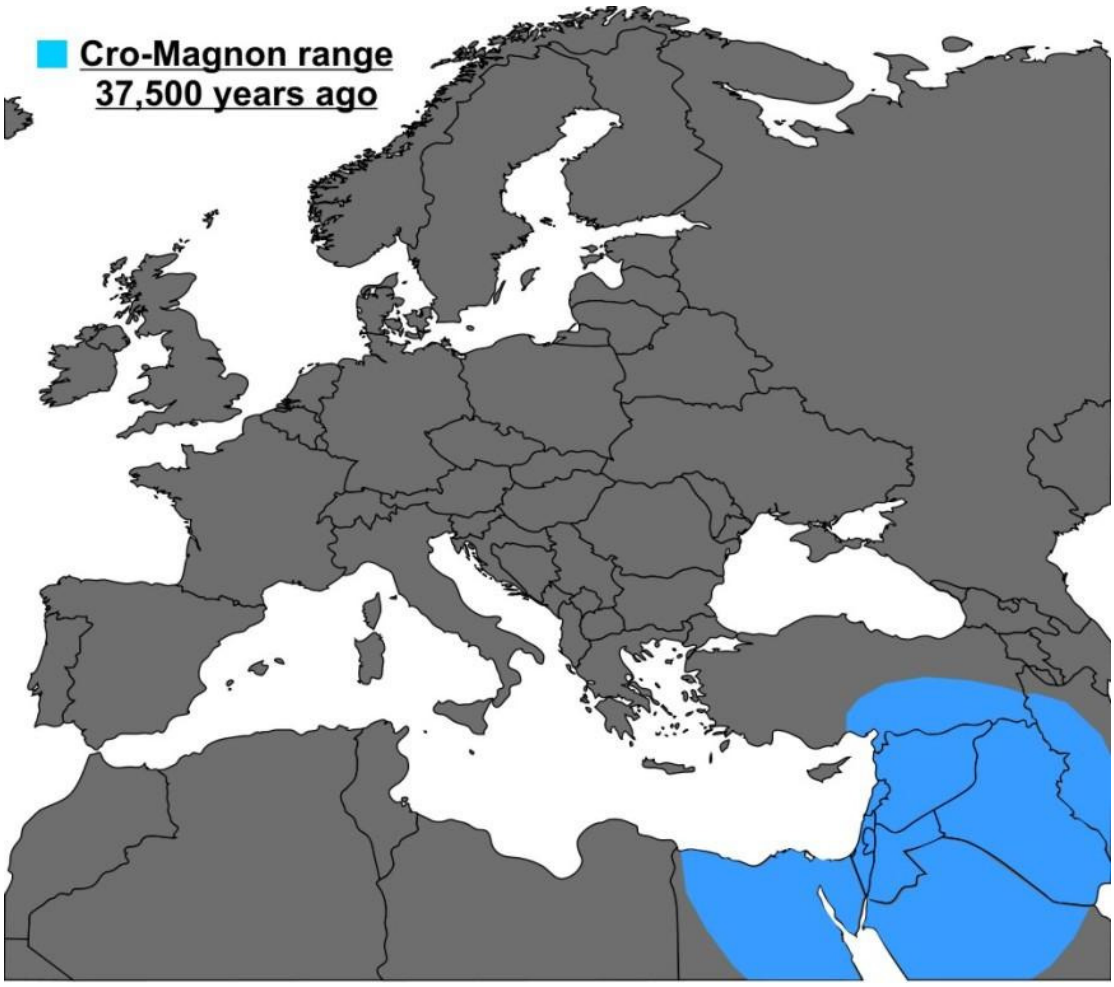
The Migration of Early Man

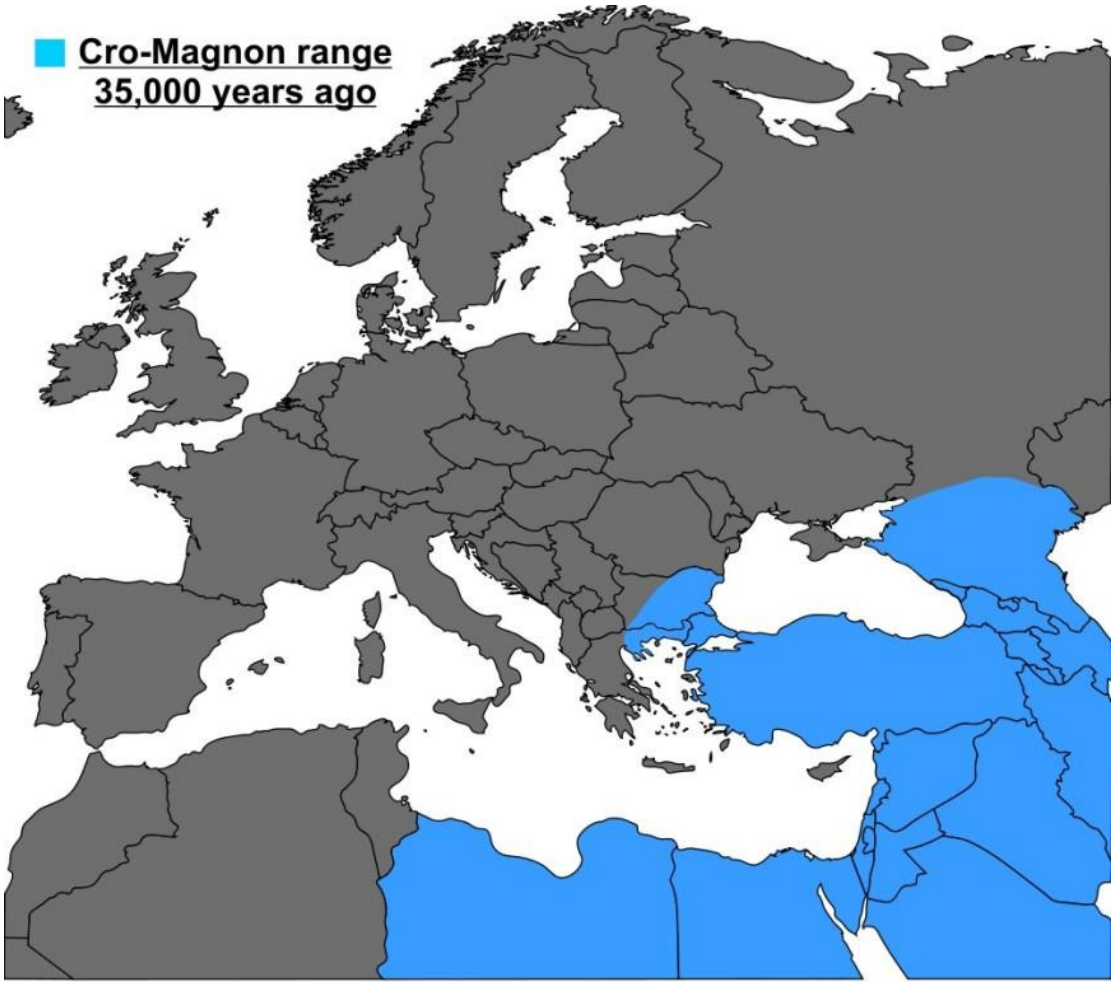
It is convenient to simplify the origins of man by grouping together all of our ape-like ancestors as Hominids, and then drawing the starting line with the rise of two distinct ancestral species: Neanderthal man and Cro-Magnon man. The earlier species, Neanderthal man, migrated to Europe approx 160 thousand years ago and appears to have died out approx 30 thousand years ago (although the Neanderthal Genome Project suggests some genes have survived to the present day through inter-breeding). The later species, Cro-Magnon man, migrated to Europe approx 40 thousand years ago, and is the ancestor of indigenous Europeans and their modern-day descendants.

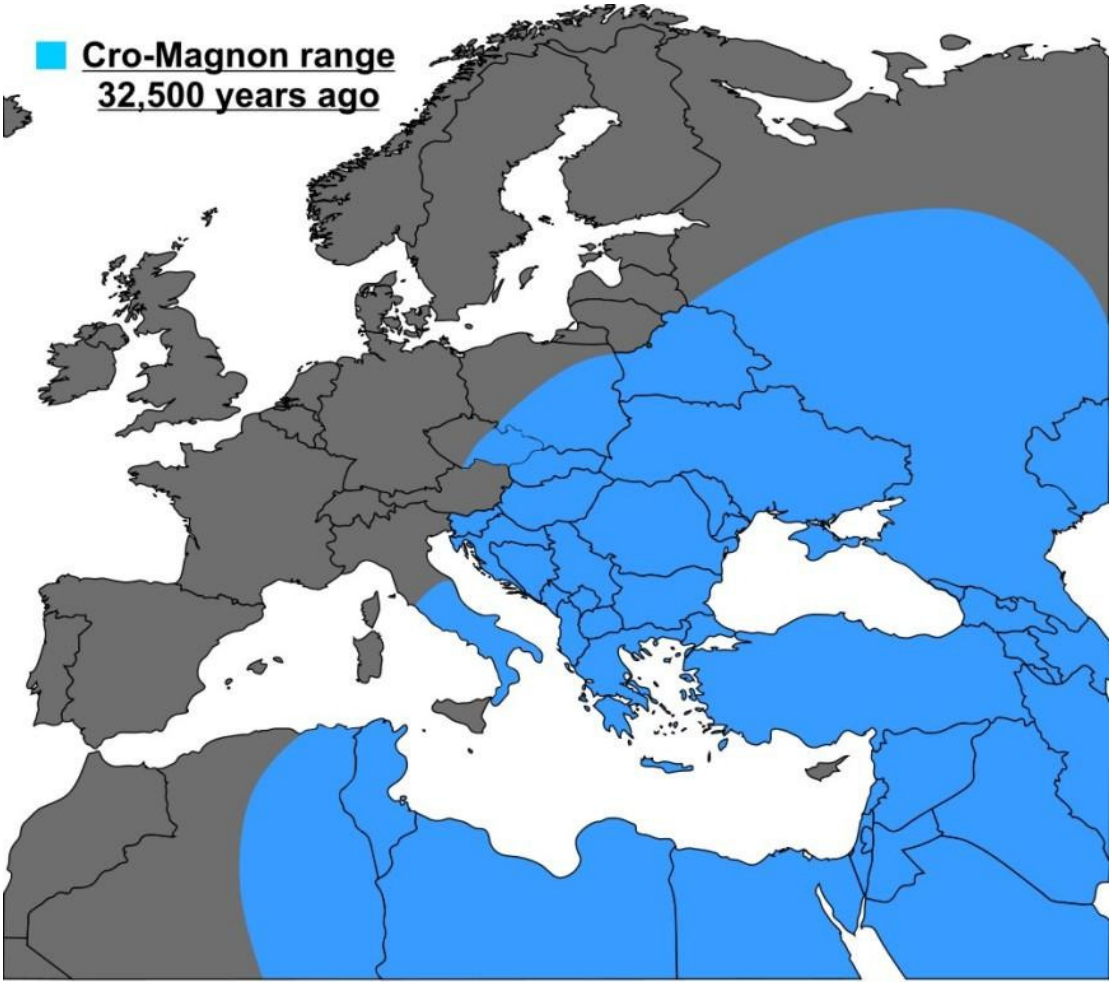


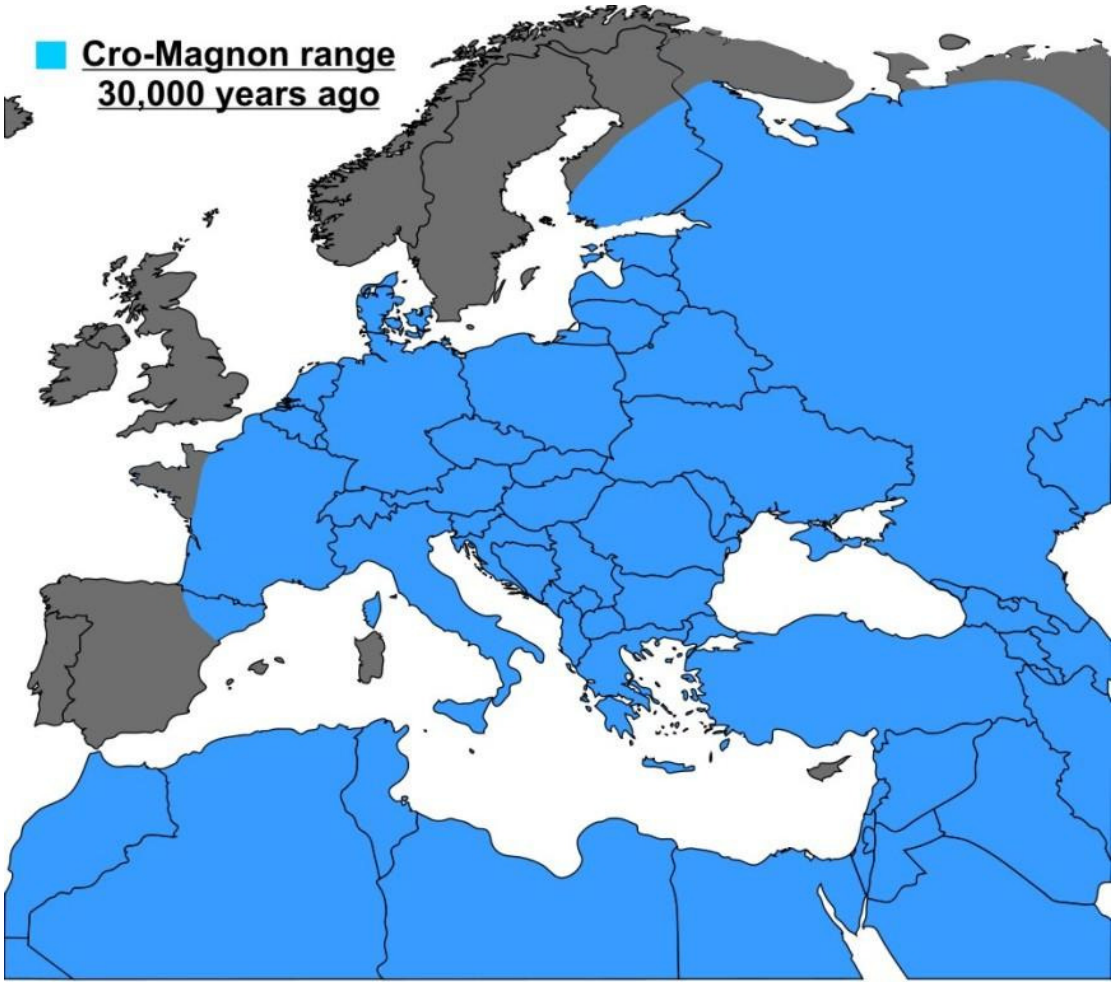
Early Migration of Homo sapiens

The migration westwards through Europe took thousands of years, and it is likely that the gradual displacement of Neanderthal man was achieved by a combination of factors such as climate change, competition for food, and tribal conflict. The slow process of displacement is charted by the following maps.

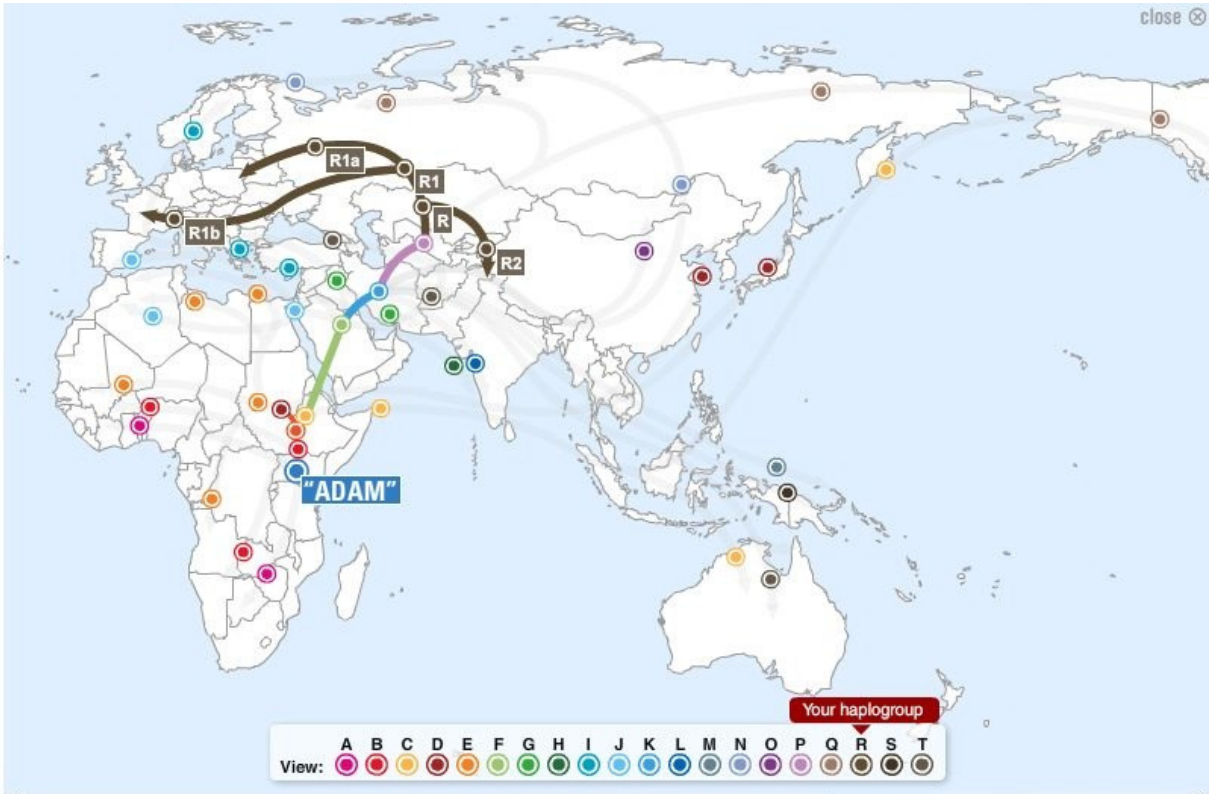

Cro-Magnon range
37,500 years ago


Cro-Magnon range
35,000 years ago


Cro-Magnon range
32,500 years ago


Cro-Magnon range
30,000 years ago

The migration of Cro-Magnon man through Europe included numerous diverse haplogroups which subdivided into subgroups and branches, and eventually settled in different locations. This is the basis for racial distinctions and, much later, national identities. Haplogroup R divided into R1 which migrated to the west, and R2 which migrated to the east. R1 in turn divided into R1a which migrated to northern Europe, and R1b which continued to the western seaboard. **The tribes of haplogroup R1b sailed to Ireland, and they are the ancestors of the Flannerys and Flannellys of Ireland.**



Migration of Haplogroup R1b: Our Ancestors