



# DNA Haplogroups Report

for

**David Hunter**

- This is a Y-DNA Haplogroup Report
- This is a Y-DNA Subclade Report

Search criteria used in this report: Y-DNA G Subclade markers

This report contains the following sections:

- Section 1. Distribution
- Section 2. Description
- Section 3. Phylogenetic Tree
- Section 4. How it works
- Section 5. Resources

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# DNA Haplogroups

Report generated by Genebase Systems and printed on Nov 7 2012, 07:16 pm

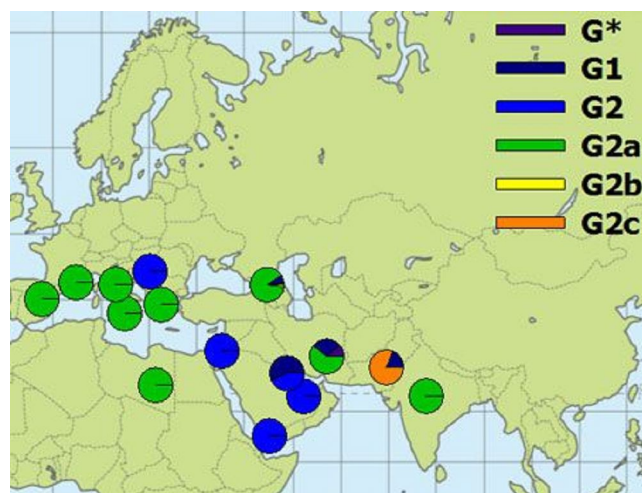
## David Hunter's Y-DNA Subclade

Based on the results of [David Hunter's Y-DNA G Subclade Test](#), David's Y-DNA Subclade is confirmed as **G2a3 (S126+)**.

## Section 1. Distribution of David Hunter's Subclade

### Geographical Distribution of the Subclades of Y-DNA Haplogroup G

Most of the genealogical analyses to date are based on Haplogroup G only, or the major subclades such as G2-P15, and therefore information on rare or newly defined subclades is somewhat limited. However, there have been some recent studies that have included a more detailed analysis of the subclades, particularly by testing for P15, the SNP that defines subclade G2. The relative proportion of the different subclades is illustrated in the map and table below lists the subclade frequencies and geographical location of populations that have been tested so far.



**Relative frequency distribution of the subclades of Haplogroup G.** The pie charts indicate the relative contribution of the different subclades in geographical areas where Haplogroup G has been detected. The G2c subclade (indicated in orange) is prevalent only in the Ashkenazi Jewish population, and G1 seems to be most predominant in Iran and the United Arab Emirates. G2, and in particular G2a, is clearly the most predominant subclade throughout Europe.

**Frequency distribution of the subclades of Haplogroup G detected worldwide.**

Country	Region or Population	Further Resolution	Frequency	N	Reference	
<b>G*</b>	Anatolian Peninsula		0.002	523	Cinnoglu et al 2004	
	Iran		0.017	117	Regueiro et al 2006	
	Isreal	Druze	0.100	20	Shen et al 2004	
	Isreal	Yemeni	0.100	20	Shen et al 2004	
<b>G1</b>	Anatolian Peninsula	G1a	0.008	523	Cinnoglu et al 2004	
	Iran	G1*	0.030	33	Regueiro et al 2006	
	Iran	G1*	0.051	117	Regueiro et al 2006	
	Pakistan		0.006	75	Sengupta et al 2006	
	United Arab Emirates		0.018	164	Cadenas et al 2007	
	United Arab Emirates	G1a	0.006	164	Cadenas et al 2007	
<b>G2</b>	Anatolian Peninsula	G2a	0.096	523	Cinnoglu et al 2004	
	Anatolian Peninsula	G2a1	0.010	523	Cinnoglu et al 2004	
	Anatolian Peninsula	G2b	0.002	523	Cinnoglu et al 2004	
	Anatolian Peninsula	G2	0.098	523	Cinnoglu et al 2004	
	Ashkenazi Jews	G2a	0.020	442	Behar et al 2004	
	North Africa	G2a	0.027	75	Alonso et al 2005	
	Crete	G2a	0.088	193	King et al 2008	
	Crete	G2a3c	0.021	193	King et al 2008	
	Druze		0.190		Hammer et al 2000	
	European Non-Jewish	G2a	0.026	348	Behar et al 2004	
	Hungary	Hungarians	0.030	100	Czányi et al 2008	
	Hungary	Szeklers	0.052	96	Czányi et al 2008	
	Spain	Gipuzkoa Basque	G2a	0.014	74	Alonso et al 2005
	Spain	Biscay Basques	G2a	0.000	72	Alonso et al 2005
	Spain	Other Basques	G2a	0.000	22	Alonso et al 2005
	Greece	Nea Nikomedeia	G2a	0.035	57	King et al 2008
	Greece	Sesklo/Dimini	G2a	0.018	57	King et al 2008
	Greece	Lerna/Franchthi	G2a	0.018	57	King et al 2008
	Greece	Sesklo/Dimini	G2a3c	0.035	57	King et al 2008
	Greece	Lerna/Franchthi	G2a3c	0.035	57	King et al 2008
	India		G2a	0.012	728	Sengupta et al 2006
	Iran	North	G2a	0.121	33	Regueiro et al 2006
	Iran	South	G2a	0.060	117	Regueiro et al 2006
	Isreal	Iraqi		0.100	20	Shen et al 2004
	Isreal	Libyan		0.100	20	Shen et al 2004
	Isreal	Moroccan		0.300	20	Shen et al 2004
	Isreal	Palestinian		0.750	20	Shen et al 2004
	Isreal	Yemeni		0.500	20	Shen et al 2004
	Italy		G2a	0.063		Di Giacomo et al 2003
	Greece		G2a	0.066		Di Giacomo et al 2003
	Non-Basque Iberians		G2a	0.040	692	Alonso et al 2005
	Non-Basque Iberians		G2a1	0.001	692	Alonso et al 2005
	Czech Republic	Klatovy	G2	0.063	48	Luca et al 2007
	Czech Republic	Pisek	G2	0.062	65	Luca et al 2007
	Czech Republic	Hradec	G2	0.041	49	Luca et al 2007
	Czech Republic	Terbic	G2	0.041	49	Luca et al 2007
	Czech Republic	Bmo	G2	0.000	46	Luca et al 2007
	Czech Republic	Total Area	G2	0.043	257	Luca et al 2007
	Pakistan		G2c	0.026	75	Sengupta et al 2006
	Qatar			0.028	72	Cadenas et al 2008
	Turkey		G2b	0.042		Cinnoglu et al 2004
	United Arab Emirates			0.018	164	Cadenas et al 2008
	Yemen			0.016	62	Cadenas et al 2008

## Section 2. Description of David Hunter's Subclade

### The subclades of Haplogroup G

Current data suggest that there are at least 19 distinct lineages, or subclades, within Haplogroup G. These subclades are smaller lineages derived from two Haplogroup G subclades: G1 and G2. There is also a subclade called G\*, but this is often referred to as a paragroup with the expectation that there are likely branches within this subclade that have yet to be determined. G1 is further divided into three subclades: G1\*, G1a, and G1b. G2 is definitely more complex and can first be separated into four lineages: G2\*, G2a, G2b, and G2c. There have been many distinct subclades detected within G2a, and they can be visualized in more detail in the "Phylogenetic Tree" section of the results.

It is important to point out that the names and relative positions of the subclades within Haplogroup G have recently been altered (in 2007/2008). The SNPs remain definitive of the same branches, and it is the branch itself that is renamed or moved. There are always new SNPs being discovered, and as these SNPs are discovered they help to increase resolution of the Y-chromosome SNP tree. Below is a list of the former subclade designations with their new names and defining SNP mutations (Table 1). This list will help immensely when referring to previous genealogical studies. Since many of the SNPs discussed here are so new, little information is known about many of the subclades. However, some information about the subclades has been summarized in Table 2, and will be further updated as new data arrive.

### Further insight from unique haplotypes

Additional insight about population history can often be reconstructed by further analysis to look for unique Y-STR haplotypes that may be indicative of specific subclades. For example, Cinnioglu et al. (2000) found that phylogeographic patterns in Haplogroup G could only be detected after Y-DNA STR haplotype analysis. Haplogroup G has repeat values on several Y-STR markers that are quite distinct from other haplogroups. These include DYS425, DYS452, DYS446, and DYF399S1 (Goff and Athey 2006). DYS425=14 was found to be strongly correlated with Haplogroup G with approximately 88% of men in this haplogroup having 14 repeats at this marker, whereas this result was very rare in other haplogroups. However, one individual from subclade G2 was tested and found to be DYS425=12. This man was from a tribal area of India and it is likely that his lineage separated from the lineage leading to the European G2. The number of repeats for DYS452 tends to be smaller in subclade G2 (ranging from 25 to 28 repeats) relative to other haplogroups (28 to 33 repeats). Again, this observation seems to be unique to G2 with four individuals from G having 31 repeats suggesting that a deletion event occurred in an individual within G2, or else was present in the founder of G2. For DYS446, the allele frequency distribution is quite different depending on the value of another marker, DYS388. This indicates the presence of subclades within G2, one with a modal value of 12 at DYS388 and another with a value of 13. Overall, the number of repeats for DYS446 tends to be greater in G2 but there is a lot of overlap with other haplogroups. The shortest allele of the marker DYF399S1 has a small number of whole repeats within Haplogroup G and a unique fractional repeat value only detected in this haplogroup.

One interesting subclade, G2c, so far seems to be restricted to the Ashkenazi Jewish population (Behar et al 2004). In fact, the distribution of G2c throughout Eastern Europe tends to correspond well with the migration and settlement of the Ashkenazi Jewish population during the 16th and 17th centuries. This subclade seems to have the following modal haplotype: DYS019=15, DYS388=12, DYS389i=14, DYS389ii=18, DYS391=10, DYS392=11, DYS393=13, DYS426=11, DYS439=15 (Behar et al 2004). In this study, 14 of 34 men had the modal haplotype with the other results only a single mutation away. In addition, it seems that this subclade also has a null value for DYS425.

**Table 1. There have been recent name changes to a number of subclades within Haplogroup G.** The previous subclade names with the corresponding new names and defining SNP mutations are provided below.

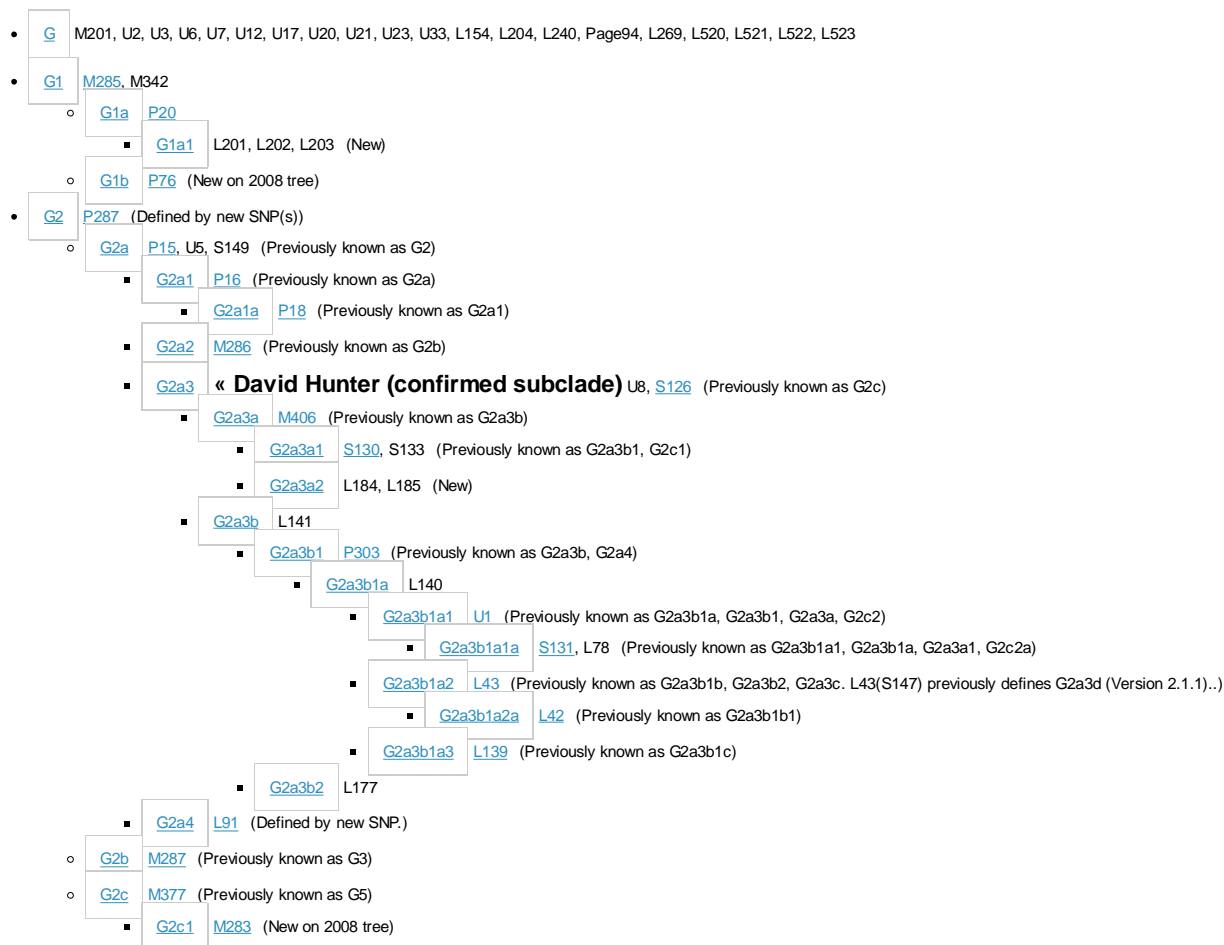
Previous Subclade	New Subclade	Defining SNPs
G2	G2a	P15, U5
G2a	G2a1	P16
G2a1	G2a1a	P17, P18
G2b	G2a2	M286
G2c	G2a3	U8
G2c1	G2a3a	U16
G2c2	G2a3b	U16
G2c2a	G2a3b1	U13
G3	G2b	M287
G5	G2c	M377

**Table 2. Summary of information currently known about the subclades of Haplogroup G.** This table represents the most up to date research data for Haplogroup G as of August 2008. As new research data becomes available in this rapidly expanding field, this table will be updated automatically.

Comments	Reference
Information about this subclade will be updated as it becomes available	
<b>G*</b>	
<b>G1</b> Uncommon in Europe	
Mostly found in Iran and United Arab Emirates	Regueiro et al 2006; Cadenas et al 2007
G1a - so far only found among four men in Turkey	Cinnoglu et al 2004
G1b - new discovered subclade about which little is currently known	
<b>G2</b>	unpublished; prediction based on Y-DNA haplotypes
G2 seems to lack a dominant modal haplotype that may indicate multiple founders	
G2a - most frequently detected subclade within Haplogroup G	
G2a - most frequent subclade in Turkey	Cinnoglu et al 2004
G2a - makes up > 80% of Haplogroup G in the Czech Republic	Luca et al 2007
G2a - second most frequent haplogroup in Crete	King et al 2008
G2a - suggested to be a good candidate marker for Neolithic migrations of farmers into Europe	Behar et al 2004 unpublished; prediction based on Y-DNA haplotypes
G2a1 - Joseph Stalin is part of this haplogroup	unpublished;
G2a3 - includes many smaller subclades and is suspected to account for most of Haplogroup G detected in Europe	prediction based on Y-DNA haplotypes unpublished data; prediction based on Y-DNA haplotypes
G2c - estimated tMRCA is 462 years ± 107	
G2c - Famous people include Newton Minow, the former chairman of the United States Federal Communications Commission and chairman of the Public Broadcasting Service, and James Franciscus, an American film and television actor	unpublished; prediction based on Y-DNA haplotypes unpublished data; prediction based on Y-DNA haplotypes
G2c - null value for DYS425 marker	
G2c - very rarely found outside of Ashkenazi Jewish men	Behar et al 2004, for example

### Section 3. David Hunter's Placement in the Y-DNA Phylogenetic Tree

SNP markers tested by Genebase =     





## Section 4. Understanding How David Hunter's Subclade is Determined

How Subclades of Y-DNA Haplogroup G are determined

The further refinement of Y-DNA ancestry can be obtained by using the Y-DNA Haplogroup G Subclade Testing Panel. This panel is based upon a collection of 11 SNPs that identify 10 different Subclades of Y-DNA Haplogroup G.

### SNP markers included in the Y-DNA Haplogroup G Subclade Panel

Location of SNP	Mutation	Subclade Defined
M201	G > T	G
M285	G > C	G1
M286	G > A	G2a2
M287	A > T	G2b
M377	A > T	G2c
P15	C > T	G2a
P16	A > T	G2a1
P18	C > T	G2a1a
P20	-C	G1a
P76	G > C	G1b
P287	G > T	G2

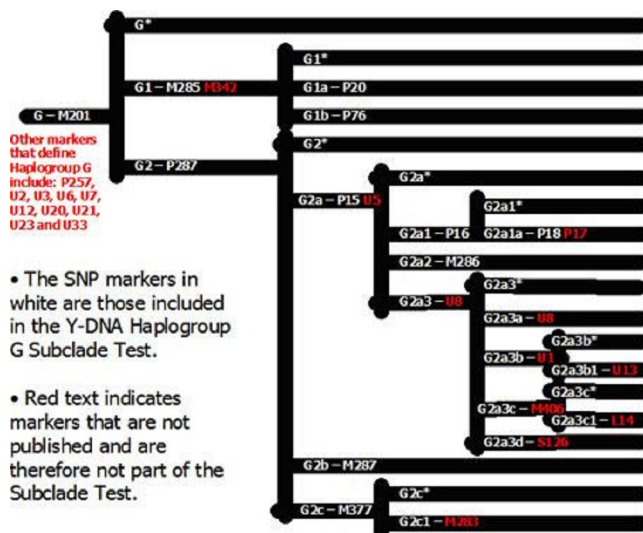
The phylogenetic tree of the subclades of Haplogroup G is illustrated below. It is current as of August 2008, but this haplogroup seems to be in a state of rapid change due to discovery of new SNPs and rearrangement of phylogenetic relationships, so it is likely that this tree will be altered in the future.

The procedure for identifying your Y-DNA Haplogroup G Subclade is as follows:

Your Y-DNA Haplogroup G Subclade will be automatically determined for you after your Subclade test is completed. However, if you are interested in finding out how your subclade was determined, just follow these steps:

#### Step 1

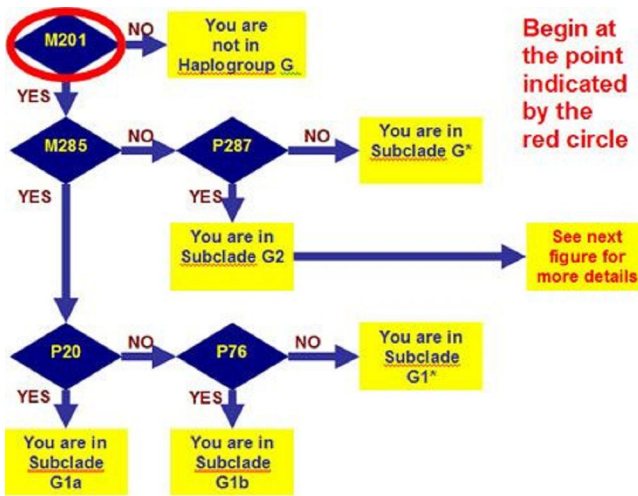
Examine your test results from the Genebase Y-DNA Haplogroup G Subclade Testing Panel. Keep track of all your positive or derived SNP states and consult the Haplogroup G Subclade phylogenetic tree diagram below.



**The phylogenetic tree of the subclades of Haplogroup G, current as of August 2008.** As the figure legend indicates, the markers in white are those markers included in the Y-DNA Haplogroup G Subclade Test Panel, whereas the markers in red have not yet published, and are therefore not included in the panel.

#### Step 2

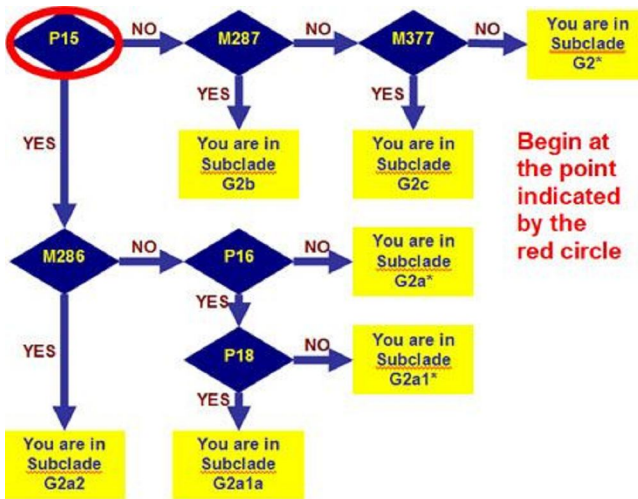
Start with the root or main branch of haplogroup G, which is ascertained by the presence of SNP M201. According to your test results, follow the branches with your SNPs from the Genebase Y-DNA Haplogroup G Subclade Testing Panel. The point at which you no longer have mutations to follow is the branch or subclade of Haplogroup G to which you belong!



Begin at the point indicated by the red circle

See next figure for more details

Once you have the results of your SNP test, you can then follow this step-by-step flow chart to determine your subclade. To begin, refer to the decision indicated with the red circle. Do you have SNP mutation M201? This should be a “yes”, otherwise you are not part of Haplogroup G. Next, determine if you have SNP M285. If you do, you are part of Subclade G1. If you have SNP mutation P20, you are part of Subclade G1a. If you do not have P20, check to see if you have P76. A positive result for P76 indicates that you are part of G1b, while a lack of P76 indicates that you are part of the G1\* lineage. Now, let’s take a step back to M285. If you lack this mutation, you are either part of Subclade G2, or G\*. A positive result for P287 indicates that you are part of G2. Please refer to the next figure for further resolution of this subclade. A negative result for P287 places you into G\*.



Begin at the point indicated by the red circle

Subclade G2 contains many deeper lineages. Again, start at the decision indicated with the red circle. Do you have SNP mutation P15? First, let’s follow the path if you are positive for P15. This mutation places you within Subclade G2a. If you are also positive for M286, you fall within Subclade G2a2. If you do not have SNP mutation M286, check if you have P16. If you do not, you are part of the G2a\* lineage. If you have P16, you are part of G2a1. Presence of SNP mutation P18 places you into G2a1a while lack of this mutation means you are part of the G2a1\* lineage. Now, let’s return to the SNP P15. If you lack this mutation, you will fall into G2b, G2c or G2\*. A positive result for M287 places you within the G2b lineage, whereas presence of M377 indicates you are part of the G2c lineage. A lack of both of these mutations indicates your classification into G2\*.



## Section 5. Resources

### Resources

[Alonso et al. \(2005\) The place of the Basques in the European Y-chromosome diversity landscape.](#) European Journal of Human Genetics 13:1293-1302.

[Bamshad et al. \(2001\) Genetic evidence on the origins of Indian caste populations.](#) Genome Research 11:994-1004.

[Barač et al. \(2003\) Y-chromosomal heritage of Croatian population and its island isolates.](#) European Journal of Human Genetics 11:535-542.

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[Cadenas et al. \(2008\) Y-chromosome diversity characterizes the Gulf of Oman.](#) European Journal of Human Genetics 16:374-386.

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[Luca et al. \(2007\) Y-chromosomal variation in the Czech Republic.](#) American Journal of Physical Anthropology 132:132-139.

[Luis et al. \(2004\) The Levant versus the Horn of Africa: Evidence for bidirectional corridors of human migration.](#) The American Journal of Human Genetics 74:532-544.

[Marchani et al. \(2008\) Culture creates genetic structure in the Caucasus: Autosomal, mitochondrial, and Y-chromosomal variation in Daghestan.](#) BMC Genetics 9:47

[Marjanovic et al. \(2005\) The peopling of modern Bosnia-Herzegovina: Y-chromosome haplogroups in the three main ethnic groups.](#) Annals of Human Genetics 69:1-7.

- [Mendizabal et al. \(2008\) Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba.](#) BMC Evolutionary Biology 8:213
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