FRENCH SURNAME DNA PROJECT RESULTS BY PERSON

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P#	FG#	M	Ancestor	Dates	Location		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
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P#	FG#	M	Ancestor	Dates	Location	Hg	393	390	19	391	385a	385b	426	388	439	389-1	392	389-2	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d	464e	464f	460	GATAH4	YCAIIa	YCAIIb	456	607	576	570	CDYa	CDYb	442	438
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1001	101		Joseph	~1726-1774	NC	R1b	13	24	14	10	11	14	12	12	13	14	13	30	16	9	10	11	11	25	16	19	29	15	15	17	18	0	0													
1012	112	3	Moses	?-<1797	NJ / PA	R1b	13	23	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	24	15	19	29	15	16	17	18	0	0													
1019	119	3	David	1746-1838	NJ	R1b	13	23	14	10	11	14	12	12	12	13	13	29	17	9	10	11	11	24	15	19	30	16	16	17	18	0	0	10	10	19	19	14	14	18	17	37	39	12	12
1003	103	3	Samuel	~1748-~1765	NC	R1b	13	23	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	24	15	19	29	15	16	17	18	0	0	10	10	19	19	14	14	18	17	36	38	12	12
1004	104	4	Gideon	1760-1836	CT / PA	R1b	12	24	14	11	11	15	12	12	12	14	13	30	17	9	10	11	11	25	14	19	29	15	15	16	16	0	0													
1013	113	3	*Aaron	1767-1850	NJ	R1b	13	23	14	11	11	14	12	12	12	12	13	28																											
1002	102	3	Richard	~1775-1838	NJ	R1b	13	23	14	11	11	14	12	12	12	13	13	29	17	9	10	11	11	24	15	19	29	15	16	17	18	0	0	10	10	19	19	14	14	18	17	37	39	12	12
1034	134	3	Samuel C.	~1790-1837	TN	R1b	13	23	14	10	11	14	12	12	13	13	13	29	18	9	10	11	11	24	15	19	29	15	16	17	18	0	0	10	10	19	19	14	14	18	17	36	37	12	12
1024	124	4	Charles	1790-1846	ENG / CAN	R1b	13	24	14	11	11	15	12	12	12	14	13	30	17	9	10	11	11	25	14	19	29	15	15	17	18	0	0													
1009	109	8	James B.	1832-1887	OH / IN	R1b	13	24	14	11	11	14	12	12	12	13	13	29	19	9	9	11	11	25	15	19	30	15	15	17	17	0	0													
1030	130	8	*James R.	~1803-1850	ENG / CAN	R1b?	12	24	14	11	11	14	12	12	12	13	13	29																											
1035	135		John	~1645-1713	NJ																																								
1007	107																																											
1020	120																																											

For More Information and To Join The French Surname DNA Project,
See Our Website: http://dnafrench.tripod.com

FRENCH SURNAME DNA PROJECT REPORT

Legend:

P = Participant, FG = Family Group, M = Match, Hap = Haplogroup

* = Needs Additional Testing

Notes:

The Family Group (FG) # is determined by the order of when your DNA Test Request was received by Family Tree DNA.

Individual Participant Test Results are posted once all results are back from the lab.

Individual Ancestor Lists are being updated and may be accessed via the First Name Link in the Ancestor Column.

Match Number, "M" Column In Table, Corresponds to the Number Listed Under Distinct French Lines.

Mutations/Differences are highlighted in YELLOW.

Matches as of 12 March 2005:

6 Exact Matches!

1-3. A 25/25 match between FG #102(Richard), FG #103(Samuel) and FG #112(Moses). In addition, there is a 35/37 Match between FG #102(Richard) and FG #103(Samuel). They are highlighted in LIGHT BLUE in the chart above.

4. A 25/25 match between FG #111(Richard), FG #114(Edward) and FG #131(Richard). They are highlighted in BRIGHT BLUE in the chart above.

5. A 25/25 match between FG #125(Samuel) and FG #126(Jacob).
They are highlighted in BRIGHT PINK in the chart above.

6. A 12/12 match between FG #132(*Martin) and FG #133(James).
They are highlighted in MEDIUM PURPLE in the chart above.

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10 Partial Matches!

1. A 24/25 match between FG #116(Thomas) and FG #102(Richard), FG #103(Samuel) and FG #112(Moses).

2. A 11/12 match between FG #113(*Aaron) and FG #102(Richard), FG #103(Samuel) and FG #112(Moses). The additional 13 or 25 markers for FG #113(*Aaron) need to be tested to establish a definitive connection.

3. A 22/25 match between FG #119(David) and FG #102(Richard), FG #103(Samuel) and FG #112(Moses).
In addition, there is a 34/37 match between FG #119(David) and FG #102(Richard).
Note: It appears that several of the lines from the Essex County, New Jersey area are related.
They are highlighted in LIGHT BLUE in the chart above.

4. A 23/25 match between FG #121(David) and FG #115(John P.).
They are highlighted in VIOLET in the chart above.

5. A 23/25 match between FG #117(Robert) and FG #118(James C.).
They are highlighted in LIGHT GREEN in the chart above.

6. A 22/25 match between FG #104(Gideon) and FG #124(Charles).
They are highlighted in BRIGHT GREEN in the chart above.

7. A 24/25 match between FG #123(William) and FG #125(Samuel) and FG #126(Jacob).
They are highlighted in BRIGHT PINK in the chart above.

8. A 11/12 match between FG #109(James B.) and FG #130(*James R.). The additional 13 or 25 markers for FG #130(*James R.) need to be tested to establish a definitive connection.
They are highlighted in MEDIUM BLUE in the chart above.

9. NOTE: There are multiple partial matches listed below for FG #132(*Martin). The match is listed with Distinct French Line #17 (MEDIUM PURPLE), however, as noted below, he could be related to several other different lines or could be a new Distinct French Line. The additional 13 or 25 markers need to be tested to establish a definitive connection.

9-A. A 11/12 match between FG #132(*Martin) & FG #102(Richard), FG #103(Samuel), FG #112(Moses). Richard, Samuel & Moses are related via Distinct French Line #3.

9-B. A 10/12 match between FG #132(*Martin) & FG #113(Aaron), FG #116(Thomas), FG #119(David). Aaron, Thomas & David are related via Distinct French Line #3.

9-C. A 10/12 match between FG #132(*Martin) & FG #124(Charles) of Distinct French Line #4 (BRIGHT GREEN), FG #109(James B.) of Distinct French Line #8 (MEDIUM BLUE) and FG #108(William) of Distinct French Line #7.

10. A 33/37 match betwenn FG #103(Samuel) & FG #134(Samuel C.) of Distinct French Line #3 (LIGHT BLUE).

17 Distinct French Lines:

01. FG #100(John)

02. FG #101(Joseph)

03. FG #102(Richard), FG# 103(Samuel), FG# 112(Moses), FG#116(Thomas), FG#119(David) and possibly FG #113(*Aaron) and possibly FG #132(*Martin).

04. FG #104(Gideon), FG#124(Charles) and possibly FG #132(*Martin).

05. FG #105(Henry)

06. FG #106(William)

07. FG #108(William) and possibly FG #132(*Martin).

08. FG #109(James B.) & and possibly FG #130(*James R.) and possibly FG #132(*Martin).

09. FG #110(John)

10. FG #111(Richard) and FG #114(Edward)

11. FG #115(John P.) & FG #121(David)

12. FG #117(Robert) & FG #118(James C.)

13. FG #122(John)

14. FG #123(William), FG #1025(Samuel) & FG #1026(Jacob)

15. FG #128(Jack)

16. FG #129(William)

17. FG #132(*Martin) & FG #133(James)

NOTE: The markers listed in BLUE in the top two rows of the table are ones that mutate faster than other ones. Please see information below from Family Tree DNA on how to interpret these changes.

"It is obvious from our observation of 1000's of samples that some markers change or mutate at a faster rate than others. While that actual 'faster rate' has not yet been definitively calculated, not all markers should be treated the same for evaluation purposes.

The markers in blue have shown a faster mutation rate then the average, and therefore these markers are very helpful at splitting lineages into sub sets, or branches, within your family tree.

Explained another way, if you match exactly on all of the markers except for one or a few of the markers we have determined mutate more quickly, then despite the mutation this mismatch only slightly decreases the probability of two people in your surname group who match 11/12 or even 23/25 of not sharing a recent common ancestor."

Source: Family Tree DNA

Haplogroups

Haplogroups are a classification tied to deep ancestry (think 10,000 or 10's of 1000's of years ago) and are used in the human Philogenetic tree. Please note that the countries in this database are the countries of the individuals that were tested. The purpose of the country information is to tell researches about migratory patterns, and should not be used to determine countries of origin.

Haplogroup Test

Your matches suggest that you belong to a particular Haplogroup. You may confirm that by ordering a Y-DNA SNP test for the particular clade or Haplogroup.

The suggested test can only determine whether you are a particular Haplogroup or not. If you are not, then additional tests would be needed to determine your haplogroup. The test can be performed on the DNA sample that you have already submitted. You may order it by logging on to your account at the FTDNA website, select Haplogroup and then the order link.

Source: Family Tree DNA

For Detailed Country Information, See your Individual FTDNA Haplogroup Results Report.

Haplogroup Descriptions

? FamilyTreeDNA is unable to suggest a probable haplogroup based on your matches. Please contact FamilyTreeDNA to discuss your Y-DNA Haplogroup.

C Haplogroup C is found throughout mainland Asia, the south Pacific, and at low frequency in Native American populations. Haplogroup C originated in southern Asia and spread in all directions. This lineage colonized New Guinea, Australia, and north Asia, and currently is found with its highest diversity in populations of India.

C2 The C2 lineage is distributed throughout the Polynesia, Melanesia, New Guinea, and Indonesia.

C3 The C3 lineage is believed to have originated in southeast or central Asia. This lineage then spread into northern Asia, and then into the Americas.

D1 This lineage is a descendent of the D lineage and is currently present in Southeast Asia and Tibet. Like its progenitor it is also found in low frequencies in Mongolian populations, but unlike D it is completely absent from Japan.

E1 This haplogroup is restricted to Africa where it occurs at intermediate frequencies. It is less common than its sister lineage E3a.

E3a Haplogroup E3a is an Africa lineage. It is currently hypothesized that this haplogroup dispersed south from northern Africa within the last 3,000 years, by the Bantu agricultural expansion. E3a is also the most common lineage among African Americans.

E3b This haplogroup is believed to have evolved in the Middle East. It expanded into the Mediterranean during the Pleistocene Neolithic expansion. It is currently distributed around the Mediterranean, southern Europe, and in north and east Africa.

G This lineage may have originated in India or Pakistan, and has dispersed into central Asia, Europe, and the Middle East. The G2 branch of this lineage (containing the P15 mutation) is found most often in the Europe and the Middle East.

I The I, I1, and I1a lineages are nearly completely restricted to northwestern Europe. These would most likely have been common within Viking populations. One lineage of this group extends down into central Europe.

I1b This line was derived within Viking / Scandinavian populations in northwest Europe and has since spread down into southern Europe where it is present at low frequencies.

J2 This lineage originated in the northern portion of the Fertile Crescent where it later spread throughout central Asia, the Mediterranean, and south into India. As with other populations with Mediterranean ancestry this lineage is found within Jewish populations. The Cohen modal lineage is found in Haplogroup J2.

N This haplogroup is distributed throughout Northern Eurasia. It is the most common Y-chromosome type in Uralic speakers (Finns and Hungarians). This lineage most likely originated in northern China or Mongolia and then spread into Siberia where it became a very common line in western Siberia.

O2 Haplogroup O2 has two primary lines, the 465 line and the M95 line. Both lines are found in Asia. The 465 line is at high frequency in Japanese and Korean populations and at low frequency in east Asia. The M95 line is found in Southeast Asian populations (Malaysia, Vietnam, Indonesia, and southern China).

P The undifferentiated P lineage is a very rare haplogroup in populations at this time. Although it was the ancestral line to haplogroups Q and R it is only found at low frequency in India, Pakistan, and central Asia with a most likely point of origin in either central Asia or the Altai region of Siberia.

Q The Q lineage is the lineage that links Asia and the Americas. This lineage is found in North and Central Asian populations as well as native Americans. This lineage is believed to have originated in Central Asia and migrated through the Altai / Baikal region of northern Eurasia into the Americas.

R1 The undifferentiated R1 lineage is quite rare. It is found only at very low frequencies in Europe, Central Asia, and South Asia. This lineage possibly originated in Europe and then migrated east into Asia.

R1a The R1a lineage is believed to have originated in the Eurasian Steppes north of the Black and Caspian Seas. This lineage is believed to have originated in a population of the Kurgan culture, known for the domestication of the horse (approximately 3000 B.C.E.). These people were also believed to be the first speakers of the Indo-European language group. This lineage is currently found in central and western Asia, India, and in Slavic populations of Eastern Europe.

R1b Haplogroup R1b is the most common haplogroup in European populations. It is believed to have expanded throughout Europe as humans re-colonized after the last glacial maximum 10-12 thousand years ago. This lineage is also the haplogroup containing the Atlantic modal haplotype.