

SNP M253 & ~300 other SNPs (I1)

SNP DF29 & 3 other SNPs (I1a)

SNP P215 & 40 other SNPs (I2)

SEE Hg I2a1 (I-L460) TREE

SNP Z17954

STRs Nominal ancestral haplotype at emergence from DF29 Block.

FTDNA Panel 1	393	390	19/394	391	385a	385b	426	388	439	389-1	392	389-2
	13	23	14	10	13	14	11	14	11	12	11	28

FTDNA Panel 2	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
	15	8	9	8	11	23	16	20	28	12	14	15	16

FTDNA Panel 3	460	GATA H4	YCA I1a	YCA I1b	456	607	576	570	CDYa	CDYb	442	438
	10	10	19	21	14	14	17	19	35	37	12	10

FTDNA Panel 4	531	578	DYF 395S1	DYF 395S1	590	537	641	472	DYF 406S1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
	11	8	15	15	8	11	10	8	9	9	12	23	25	15	10	12	12	16	8	13	25	20	13	13	11	12	11	11	12	11

FTDNA Panel 5	710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	GATA A10	463	441	GGAA T 1B07	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
	32	12	8	17	12	24	27	19	11	12	12	13	11	9	11	11	10	11	12	31	11	13	21	16	11	10	22	15	19	11	25	17	12	16	25	12	22	18	12	14	18	9	12	11

LEGEND:

a) Mutation notations

SNPs and InDels are denoted in bold type face. STR markers are denoted in light type face. The 'DYS' of DYS-prefixed STR markers is omitted; prefixes for all others are shown with a more detailed notation (e.g. DYF395S1a, DYR33, YCaIib, (Y-)GGAAT 1B07, FTY371).

b) Participant kit number and testing details:

No. of STR markers examined (e.g. Y-DNA37, 67 or 111 at FTDNA).
 561 (-n): Y-DNA111 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
 517 (-n): Y-DNA67 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
 487 (-n): Y-DNA37 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
 The number of markers examined is increased by 277 (e.g. from 561 to 838) where FTDNA has included a Panel 7 (P7) extraction of data from a Big Y test. In this case n = total number of no calls at the 727 loci of the extraction. Where this is subsequent to an earlier extraction, information on no calls may be shown for both.

111 BY: Has taken the original BigY or later Big Y-500 test, and / or BY-700 = has taken a Big Y-700 test (whether or not an earlier Big Y test was taken)
 YE = has taken a Y Elite test with FGC
 PNL = has taken an FTDNA R1b SNP Pack Test or YSeq R1b Panel Test
 NG = has taken a Nat Geographic Geno 2.0 or later test contributing to the analysis.

Grey shading indicates that results are not yet available or have not yet been reviewed.
 Light grey shading indicates preliminary review only of results undertaken.

Surname in parenthesis if no 'distant paternal ancestor' surname identified.
 *Pseudonymised or totally anonymised tester identity (see 'Important Notices', items 5 and 6).

c) STR Mutation highlighting (frequencies revised February 2020 in accordance with Fig 4a at <https://mccarthydna.wordpress.com/>):

Very slow moving* STR markers (very low mutation rates) or rare multi-step mutation
 Slow moving STR markers (low mutation rates)
 Postulated STR back-mutation

Not generally applied to P6 or P7 (see (d) below).

d) Other

> is used to denote a change in status (no. of repeating motifs) at an STR locus, e.g. 576: 18>17 indicates a mutation from 18 to 17 at DYS 576. Elsewhere (in dates) it is used to indicate "later than".

P4 STR marker in FTDNA Panel 4 (38th - 67th markers in FTDNA sequence).
 P5 STR marker in FTDNA Panel 5 (68th - 111th markers in FTDNA sequence).
 P6 STR marker in FTDNA Panel 6 (112th - 561st markers in FTDNA sequence, extracted from Big Y data).
 P7 STR marker in FTDNA Panel 7 (562nd - 838th markers in FTDNA sequence, extracted from Big Y data).

(A(A)NNN(NN)N)±/- Results of individual SNP testing (positive / negative), or extracted from a Next Generation Sequencing (NGS) test such as Big Y or Y Elite 2.1, or a Pack or Panel Test, where of particular relevance to kits close by on the tree.

IMPORTANT NOTICES

- The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA) for which thanks are duly given. Some recent subclade identification may come from testing at YSeq or elsewhere.
- The tree serves those McCarthys (or variants of the name) in Haplogroup I1, that headed by SNP I-M253, with its numerous equivalents. An approximate ancestral haplotype at the time of emergence from the I-DF29 SNP 'Block' has been evaluated. For the fast mutating STR markers CDYa/b and DYS712 its allele values are nominal, but others may also be erroneous. This haplotype is nonetheless used as a basis for an indication of STR mutations which have occurred from this point down to the present day. To provide such information, data has been mined from the I1 Eastern Europe and I1-S4795 Projects and a variety of surname projects, including but not limited to those for the names Gardner, Graham, Lancaster, May, Peters, Shiver and Terry. In this respect, thanks are due to the haplotype owners and their project administrators for making their data available in the spirit of 'citizen science' for the mutual benefit of all concerned. Participant identities abide by the criteria of (5) below.
- The overall tree structure is given for background information to show where the tested or predicted SNPs for the McCarthys (and variants thereof) fall. It generally follows FTDNA's Haplotype as it stood early in 2021. The number of equivalent SNPs in each 'block' gives an idea of the length of time between each level on the tree. For the mostpart, only those SNP blocks pertinent to the phylogeny of the McCarthys are shown. It is recognised that FTDNA's Haplotype is a live document and may be subject to development at any time. Responsibility for any errors arising from interpretation of data or failure to update to the latest available information rests solely with the Owners of this tree, the McCarthy Surname Study analysts.
- The tree combines relationships based on STR testing with firm definition afforded by SNP testing. Where configurations are not confirmed by SNP testing, different permutations are possible. The reliability can only be improved by more participants testing STRs to 111 markers and Next Generation Sequencing (NGS) testing such as FGC's Elite 2.1 and FTDNA's Big Y-700, identifying SNPs which give firm definition to the branches and twigs (subclades) of the tree.
- The 'pseudonymised' format of FTDNA kit no. plus Most Distant Known Paternal Ancestor (MDKA) surname (or where the latter is not available the tester's surname or simply the kit no.) has been used for tester identity where the participant or his kit manager:
 - has opted in to allowing publication of his "pseudonymized DNA results and ancestor information in the public results pages" (and for data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet) OR
 - has e-mailed to a McCarthy Surname Study analyst permission to display the output from the analysis of data from any source in the tree (see (6) and (7) below) OR
 - has made results available to others (e.g. depositions in the 'Y-DNA Warehouse') in the knowledge their analyses, identifiable with surname and / or kit number, would be placed in the public domain.
 Otherwise identities of testers will be 'totally anonymised' with an 'XHgl-' series 'dummy' reference number known only to the McCarthy Surname Study analysts.
- Status of a participant's FTDNA privacy setting has been determined in a one-off exercise on or since 25 May 2018 (or for recent testers, at the time a kit has been added to the tree). Should a participant / kit manager wish the tree respect a subsequent alteration to the setting or indeed have a kit removed altogether and any back-up records held by the McCarthy Study analysts expunged, will he / she please request this by e-mail. (See (7)).
- Despite the option at 5 (a) having been selected in a participant's FTDNA Project Preferences, certain data to which the McCarthy Surname Study analysts may have access, e.g. FTDNA Panels 6 and 7 STRs extracted from Big Y testing, results of testing elsewhere, may not be available, or readily available, in the public domain. Inclusion of output from analysis of such data on the tree requires e-mailed authorisation using an appropriate form of words which can be supplied to the participant or his kit manager. See (7) for contact details.
- For the identity and contact details of the McCarthy Surname Study analysts responsible for this tree please go to <https://www.familytreedna.com/groups/mccarthy-surname-study/about>.

NOTES: (Not all may currently be in use)

- Where SNP / InDel Y-chromosome positions are cited, these relate to Human Reference Genome 'Build 38' (hg38 / GRCh38).
- Where tested.
- Within groups of 'equivalent' SNPs and / or associated STRs, the mutations could have occurred in any order.
- Mutation(s) may have occurred further up the tree.
- Reported SNP in the 125 bp repeat region known as DYI19; may be unreliable and difficult or impossible to confirm by Sanger Sequencing.
- A defining SNP or InDel appears to exist on the Y-chromosome, but its location is uncertain. (Frequently this is because it is on a palindromic arm). Unlikely to be suitable for individual (Sanger Sequence) testing.

MCCARTHY (Y-DNA) SURNAME STUDY

PHYLOGENETIC TREE FOR MCCARTHYS IN HAPLOGROUP I1 (I-M253)

Last updated - 04 March 2021

